ORGANISM: Artificial Sequence

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Sequence 4651, Application US/10289762
GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmen:
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pre
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
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) Sequence 5845, Application US/10289762
(GENERAL INFORMATION:
) APPLICANT: Griffals, R.
) TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmen TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, profitting of INVENTION: and treatment of infection
) TITLE OF INVENTION: and treatment of infection
) TITLE PEPRENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/10/289,762
) CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
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GENERAL INFORMATION:

APPLICANT: Wood, Linda

APPLICANT: Wagner, Susanne

APPLICANT: Parodi, Luis

TITLE OF INVENTION: Single Nucleotide Polymorphisms in GH-1

FILE REFERENCE: 00791.US;

CURRENT APPLICATION UNMER: US/10/289,845

CURRENT FILING DATE: 2002-11-07

NUMBER OF SEQ ID NOS: 51

SOFTWARE: PatentIn version 3.1

SEQ ID NO 14

LENGTH: 20
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Pred. No. 4.9e+02;
0; Mismatches 3;
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O.7%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3;
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CGAACGGTAGAAATCCAAG 19
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; ORGANISM: Chlamydia pneumoniae
US-10-289-762-4651
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Best Local Similarity 84.2%;
Matches 16; Conservative
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 2388
LENGTH: 20
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                                                       ; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA US-10-266-090-43821
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Pred. No. 4.9e+02;
0; Mismatches 3; Indels
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APPLICANT: BONAN, CAROLINE
APPLICANT: COLDERT, MICHELLE
APPLICANT: COLDERT, MICHELLE
APPLICANT: WANG, RONG-LIN
TITLE OF INVENTION: CERRAL TRINUCLECTIDE SIMPLE SEQUENCE
TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
CURRENT APPLICATION NUMBER: US 10/266,090
CURRENT APPLICATION NUMBER: US 60/326,117
PRIOR APPLICATION NUMBER: US 60/326,117
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 51812
SOFTWARE: Fastes of for Windows Version 4.0
SEQ ID NO 47293
LENGTH: 20
                                                                                                                                                                                                                                            3; Indels
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0.7%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3;
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APPLICANT: GOFF, STEPHEN
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84.2%;
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Best Local Similarity 84.2.
"Thes 16; Conservative
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Best Local Similarity 84.2%
Matches 16, Conservative
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US-10-289-762-2388
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963 CCAACGGTGGAAGTCCAAG 981

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APPLICANT: RosettaGemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT PILLORATION WIDMER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 48869
LENGTH: 20
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GENERAL INFORMATION:
APPLICANT: RosettaGemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GE
TITLE OF INVENTION: USES THERROF
FILE REFERENCE: 47487
CURRENT APPLICATION WUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
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SEQ ID NOS: 86841
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GENERAL INFORMATION:
APPLICANT: Rosettademonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY (TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
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Pred. No. 4.9e+02;
0; Mismatches 3;
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Pred. No. 4.9e+02;
0; Mismatches 3;
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Best Local Similarity 84.2%; Pred. No. 4.9e+02;
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Best Local Similarity 84.2%;
Matches 16; Conservative (
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Best Local Similarity 84.2%;
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US-10-310-188-48869
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-310-188-64522
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US-10-310-188-59951/c
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LENGTH: 20
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
TITLE OF INVENTION: THEREOF
FILE REPERRINCE: 45282
CURRENT APPLICATION NUMBER: US/10/293,338
CURRENT FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 8785
SOFTWARE: Patentin version 3.1
LENGTH: 20
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
FILE REPERENCE: 47416
CURRENT APPLICATION NUMBER: US/10/303,778
CURRENT APPLICATION NUMBER: US/10/303,778
NUMBER OF SEQ ID NOS: 17603
SOFTWARE: Patentin version 3.1
SEQ ID NO 1350
LENGTH: 20
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Pred. No. 4.9e+02;
0; Mismatches 3; Indels
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14.2%; Pred. No. 4.9e+02;
ve 0; Mismatches 3; Indels
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0.7%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                      RESULT 709
US-10-293-338-5780/c
; Sequence 5780, Application US/10293338
; GENERAL INFORMATION:
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          ORGANISM: artificial sequence
                                                                                                          Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
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Best Local Similarity 84.2%;
Matches 16; Conservative
                           FEATURE:
CTHER INFORMATION: primer
US-10-289-845-14
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US-10-293-338-5780
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US-10-310-188-48869/c
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US-10-303-778-1350
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Sequence 75, Application US/10380126
GENERAL INFORMATION:
APPLICANT: 161s Pharmaceuticals, Inc.
APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENEE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-1 EXPRESSION
FILE REPERENCE: RISP-0175
CURRENT FILING DATE: 2003-03-01
FRIOR APPLICATION NUMBER: 09/657,042
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 88
SEG ID NO 75
LENGTH: 20
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; OTHER INFORMATION: upstream amplification primer 99-24210 for SEQ 3182,
US-10-349-143-7116
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       PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 7116
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APPLICANT: Donna T. Ward
APPLICANT: William Gaarde
APPLICANT: Exert P. Monia
APPLICANT: Brett P. Monia
APPLICANT: BARET MATISENSE MODULATION OF MEKK4 EXPRESSION
TITLE OF INVENTION: ANTISENSE MODULATION OF MEKK4 EXPRESSION
TITLE OF INVENTION: ANTISENSE WOULATION OF MEKK4 EXPRESSION
CURRENT APPLICATION NUMBER: US/10/371,474
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US/09/676,436
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 69
LIENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
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84.2%; Pred. No. 4.9e+02;
tive 0; Mismatches 3;
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0.7%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3;
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, OTHER INFORMATION: Antisense Oligonucleotide
US-10-371-474-69
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US-10-371-474-69
; Sequence 69, Application US/10371474
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 16, Conservative
                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo Sapiens
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                                                                                                                                                                LENGTH: 20
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TITLE OF INVENTION: Modulation of Estrogen-Responsive Finger Protein Expression
FILE REPERENCE: RTS-0473
CURRENT APPLICATION NUMBER: US/10/317,277A
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 168
SOFTWARE: Patentin version 3.2
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Modulation of Estrogen-Responsive Finger Protein Expression
FILE REFERENCE: RTS-0473
CURRENT APPLICATION NUMBER: US/10/317,277A
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 168
SSQ ID NO 142
LENGTH: 20
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APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chimakov, Ilya
FILE OF INVENTION: Biallelic markers for use in constructing a high density...
CURRENT APPLICATION NUMBER: US/10/349,143
CURRENT APPLICATION NUMBER: US/99422,978
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
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84.2%; Pred. No. 4.9e+02;
ative 0; Mismatches 3; Indels
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                                                                                                                                              Sequence 67, Application US/10317277A GENERAL INFORMATION:
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cccagccccagccccrcc 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial
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Best Local Similarity
Matches 16; Conserv
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LENGTH: 20
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Query Match 0.7%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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Best Local Similarity
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Sequence 4, Application US/10394058

GENERAL INFORMATION:
APPLICANT: Althaus, Harald
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: Human Procalcitonin and the Preparation and Use Thereof
FILE REFERENCE: 05552.1445-00
CURRENT PELING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US/09/742,373
PRIOR APPLICATION NUMBER: 195/09/742,373
PRIOR PILING DATE: 1999-12-22
PRIOR PILING DATE: 1000-04-03
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 4
IENGTH: 20
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APPLICANT: Rark J. Graham
TITLE OF INVENTION: ANTISENSE MODULATION OF C-REACTIVE PROTEIN EXPRESSION
TITLE OF INVENTION: ANTISENSE MODULATION OF C-REACTIVE PROTEIN EXPRESSION
FILE REFERENCE: ISPH-0692
CURRENT APPLICATION NUMBER: US/10/483,424
CURRENT FILING DATE: 2004-01-22
PRIOR FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 63
SEQ ID NO 42
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.7%; Score 14.2; DB 1; Length 20; larity 84.2%; Pred. No. 4.9e+02; Conservative 0; Mismatches 3; Indels
                                                                                                           Length 20
                                                                                                                                                 Indels
                                                                                                    Query Match 0.7%; Score 14.2; DB 1; Best Local Similarity 84.2%; Pred. No. 4.9e+02; Matches 16; Conservative 0; Mismatches 3;
                                  ; OTHER INFORMATION: Antisense Oligonucleotide US-10-380-126-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Antisense Oligonucleotide US-10-483-424-42
                                                                                                                                                                                    1012 CCTGAAAAGAGGGGGAGC 1030
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ORGANISM: Artificial Sequence
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ORGANISM: Unknown Organism
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Best Local Similarity
Matches 16; Conserv
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US-10-483-424-42
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RESULT 721

US-60-164-320-11958

US-60-164-320-11958

Sequence 11958, Application US/60164320

GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
TILE OF INVENTION: Xanthomous campestris Genome Sequences and Uses Thereof
FILE REPERINCE: 38-10(15804)A

CURRENT APPLICATION NUMBER: US/60/164,320

CURRENT PILING DATE: 1999-11-10

NUMBER OF SEQ ID NOS: 18992

SEQ ID NO 11958
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GENERAL INFORMATION:

APPLICANT: Bower, Scanley G.

APPLICANT: Hinkle, Gregory J.

TITLE OF INVENTION: Xanthomonas campestris Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10 (15804) A.

CURRENT FILING DATE: 1999-11-10

SEQ ID NO 14782

LENGTH: 20

LENGTH: 20
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APPLICANT: Bower, Stanley G.
APPLICANT: Hinkle, Gregory J.
TITHE OF INVENTION: Kanthemonas campestris Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(1504)B
CURRENT APPLICATION NUMBER: US/60/183,791
CURRENT FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 18992
SEQ ID NO 11958
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Length 20;
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Pred. No. 4.9e+02;
0; Mismatches 3; Indels
                                             Indels
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Score 14.2; DB 1;
Pred. No. 4.9e+02;
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Pred. No. 4.9e+02;
0; Mismatches 3;
                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 11958, Application US/60183791; GENERAL INFORMATION:
                                                                                    1091 TCACCCCCCCCCTGGGCTT 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1184 CCCGCAGAGGTGGCACC 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCCCAGTTCCACCTTCAC 1136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Xanthomonas campestris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Xanthomonas campestris US-60-164-320-14782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTCCAATTCCAGCTTCAC 19
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Best Local Similarity 84.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE NIXON & VANDERHYE P.C.
STREET 1100 NORTH GLEBE ROAD
CITY: ARLINGANA
CITY: ARLINGANA
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                      0
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MAERIENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 18;
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100.0%; Pred. No. 4.7e+02;
iive 0; Mismatches 0;
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Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: BP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-0ct-1998
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 14; DB ilarity 100.0%; Pred. No. 4.5 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 276:
US-09-155-885A-276
                                      FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PATENTIN VERBION 3.1
SEQ ID NO 9791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFREENCE DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-155-885A-276/c
; Sequence 276, Application US/09155885A
; GENERAL INFORMATION:
APPLICANT: STUTYER, LIEVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                 USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 18 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTCACCCCCACCC 3
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                        TYPE: DNA
CORGANISM: Homo sapiens
US-10-310-188-9791
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Best Local Similarity
              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                14;
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GENERAL GENERA
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bower, Stanley G.
APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Xanthemonas campestris Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15804)B
CURRENT APPLICATION NUMBER: US/60/183,791
CURRENT FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 18992
SEQ ID NO 14782
LENGTH:: 20
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                                                                                                                                            Score 14.2; DB 1;
Pred. No. 4.9e+02;
0; Mismatches 3;
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Pred. No. 4.9e+02;
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                          1184 CCCGCAGAGAGAGCACC 1202
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LENGTH: 20
TYPE: DNA
ORGANISM: Xanthomonas campestris
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Best Local Similarity 100.0%; Pr
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84.2%;
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ilarity 84.2%;
Conservative
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                                                                                                                                         Query Match 0.7
Best Local Similarity 84.2
Matches 16; Conservative
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Best Local Similarity
Matches 16; Conserv
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-10-310-188-60224/c
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US-10-310-188-9791/c
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                                                                                      US-60-183-791-11958
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LENGTH: 16
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STATE: VIRGINIA
CONTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/606,879
FILING DATE: 27-JUM-2003
CLASSIFICATION: cUnknown>
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TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
                                                                                                                                                                                                                                          Score 14; DB 1; Length 18; Pred. No. 4.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; Score 14; DB 1; Length 18; 100.0%; Pred. No. 4.7e+02;
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 276:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 276:
US-10-606-879-276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-606-879-276/c; Sequence 276, Application US/10606879; GENERAL INFORMATION:
APPLICANT: STUYYER, LIEVEN
                                                                                                                                                                                                                        0.6%; Scor.
100.0%; Pre
                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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                    LENGTH: 18 base pairs
                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                               728 GCCAGGAGAACAG 741
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Best Local Similarity
Matches 14; Conserva
                                                                                                                                                    ANTI-SENSE: NO
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Best Local Similarity
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                                                                                                                                                                                               US-10-453-792-276
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                                                                                                                                                        Sequence 5255, Application US/10310188
GENERAL INFORMATION:
APPLICAMT: ROSELTAGEMICS
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE PATENTIN VERSION 3.1
SEQ ID NO 52565
LENGTH: 18
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROSSAU, RUDI
MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 18;
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4.7e+02;
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APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-7un-2003
CLASSIFICATION: -Unknown-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-0ct-1998
APPLICATION NUMBER: PCT/EP97/02002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 0.6%; Score 14; DB 1 Similarity 100.0%; Pred. No. 4.7 14; Conservative 0; Mismatches
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APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: SADOFF, B.J.

REGISCHAFION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 276:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 276, Application US/10453792 GENERAL INFORMATION:
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COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: STUYVER, LIEVEN ROSSAU, RUDI
           728 GCCAGGAGAACAG 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       876 CTCAGGCACCACAG 889
                                                  18 GCCAGGAGAACAG 5
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                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-52565
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Best Local Similarity
Matches 14; Conserv
                                                                                                                  RESULT 728
US-10-310-188-52565/c
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US-10-453-792-276/c
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; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region PCT-US03-05326-568
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pharmacia Corporation
APPLICANT: Rose, Stuart A
TITLE OF INVENTION: Antisense Modulation Of Acyl-CoA Synthetase 1 Expression
FILE REFERENCE: 01294/1/PCT
CURRENT APPLICATION NUMBER: PCT/US03/25389
CURRENT FILING DATE: 2003-08-14
PRIOR FILING DATE: 2002-08-14
PRIOR FILING DATE: 2002-08-14
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Pred. No. 5.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 19;
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SEQUENCE 12, Application PC/TUS0117936
GENERAL INFORMATION:
TITLE OF INVENTION: FUSION OF JAZE1 AND JAZ1 GENES;
TITLE OF INVENTION: ENDOMETRIAL STROWAL TUMORS
TITLE OF INVENTION: ENDOMETRIAL STROWAL TUMORS;
FILE REFERENCE: 05311-024W01
CURRENT PAPLICATION NUMBER: PCT/US01/17936
CURRENT FILING DATE: 2001-06-04
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FRESEG FOR WINDOWS VERSION 4.0
SEQ ID NO 12
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14; DB 1;
Pred. No. 5e+02;
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100.0%; Pred. No. ...
0; Mismatches
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PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-08-29
PRIOR PLING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR FILING DATE: 2002-09-09
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 677
SOFWARE: PATENTIN VUMBER: US 60/440,129
FRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 677
SEQ ID NO 568
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 71.4%;
Matches 10; Conservative
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Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sirna Therapuetics
APPLICANT: Sirna Therapuetics
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Beigedman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of MYC and MYB
TITLE OF INVENTION: Expression or Expression of Genes Involved in the MYC and TITLE OF INVENTION: Expression or Expression of Genes Involved in the MYC and TITLE OF INVENTION: Expression or Expression of Genes Involved in the MYC and MYB
TITLE OF INVENTION: Expression or Expression of Genes Involved in the MYC and MYB
TITLE OF INVENTION: Expression or Expression of Genes Involved in the MYC and MYB
FILE REFERENCE: 400/079 (MMHB 02-1105-A)
CURRENT APPLICATION NUMBER: US 60/418,655
PRIOR FILING DATE: 2002-10-15
PRIOR FILING DATE: 2002-02-20
PRIOR FILING DATE: 2002-03-11
PRIOR FILING DATE: 2002-03-11
PRIOR FILING DATE: 2002-03-11
PRIOR FILING DATE: 2002-09-05
PRIOR FILING DATE: 2003-01-01
PRIOR PRIOR FILING DATE: 2003-01-01
PRIOR FILING DATE: 2003-01-01
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GENERAL INFORMATION:
APPLICANT: Sirna Therapuetics
APPLICANT: Sirna Therapuetics
APPLICANT: Sirna Therapuetics
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of MYC and MYB Gene
TITLE OF INVENTION: Expression of Enes Involved in the MYC
TITLE OF INVENTION: Pathways Using Short Interfering Nucleic Acid (sina)
FILE REFERENCE: 400/079 (MBHB 02-1105-A)
FURRENT APPLICATION NUMBER: DC 40/418,655
PRIOR APPLICATION NUMBER: US 60/418,655
PRIOR APPLICATION NUMBER: US 60/318,580
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR APPLICATION NUMBER: US 60/353,124
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                   Indels
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100.0%; Pred. No. 5e+02;
ative 0; Mismatches 0;
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                   Mismatches
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PCT-0803-05326-389/c
; Sequence 389, Application PC/TUS0305326
; GENERAL INFORMATION:
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SEQ ID NO 389
LENGTH: 19
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                                                                     728 GCCAGGAGAACAG 741
                                                                                                                                  18 GCCAGGAGAACAG 5
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                   14; Conservative
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Matches 14; Conserv
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               Matches
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Sequence 1315, Application PC/TUS0325389
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bharmacia Corporation
APPLICANT: Branacia Corporation
APPLICANT: Branacia Corporation
APPLICANT: Boss, Stuart A
TITLE OF INVENTION: Antisense Modulation Of Acyl-CoA Synthetase 1 Expression
FILE REPERENCE: 01294/1/PCT
CURRENT APPLICATION NUMBER: PCT/US03/25389
CURRENT FILING DATE: 2003-08-14
PRIOR FILING DATE: 2003-08-14
NUMBER OF SEQ ID NOS: 3624
SOFTWARE: Parentin version 3.2
IENGTH: 20
                                      Gaps
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100.0%; Pred. No. 5.2e+02;
tive 0; Mismatches 0; Indels
                                      Indels
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100.0%; Pred. No. 5.2e+02;
ive 0; Mismatches 0; Indels
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US-09-874-162A-12

Sequence 12, Application US/09874162A

GENERAL INFORMATION:
APPLICANT: Koentz, Jason
TITLE OF INVENTION: FUSION OF JAZFI AND JJAZI GENES IN
TITLE OF INVENTION: ENDOMETRIAL STROMAL TUMORS
FILE REPERRECE: 0531-024001
CURRENT APPLICATION NUMBER: US 09/874,162A
CURRENT FILING DATE: 2001-06-04
PRIOR PILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 12
LENGTH: 20
           100.0%; Pred. No. 5.2e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                             735 GAAACAGAACACCG 748
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                                                                                                                   18 GAACAGAACACCG 5
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           Best Local Similarity 100.
Matches 14; Conservative
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Best Local Similarity 100.0
Matches 14, Conservative
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Matches 14; Conserv
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US-10-266-090-39932
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GENERAL INFORMATION:
APPLICANT: Pharmacia Corporation
APPLICANT: Pharmacia Corporation
APPLICANT: Ross, Stuart Antisense Modulation Of Acyl-CoA Synthetase I Expression
TITLE OF INVENTION: Antisense Modulation Of Acyl-CoA Synthetase I Expression
FILE REFERENCE: 01294/1/PCT
CURRENT APPLICATION NUMBER: PCT/US03/25389
CURRENT FILING DATE: 2003-08-14
PRIOR FILING DATE: 2002-08-14
NUMBER OF SEQ ID NOS: 3624
SOFTWARE: Patentin version 3.2
SEQ ID NO 1106
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Pharmacia Corporation
APPLICANT: Pharmacia Corporation
APPLICANT: Ross Stuart Artisense Modulation Of Acyl-CoA Synthetase 1 Expression
TITLE OF INVENTION: Antisense Modulation Of Acyl-CoA Synthetase 1 Expression
FILE REFERENCE: 0129411/PcT
CURRENT APPLICATION NUMBER: PCT/US03/25389
CURRENT FILING DATE: 2003-08-14
PRIOR APPLICATION NUMBER: 60/403,591
PRIOR FILING DATE: 2002-08-14
NUMBER: PEQ ID NOS: 3624
SOFTWARE: PatentIn version 3.2
SEQ ID NO 653
LENGTH: 20
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100.0%; Pred. No. 5.2e+02;
tive 0; Mismatches 0; Indels
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CTHER INFORMATION: human ACS-1 antisense PCT-US03-25389-653
                                                                                                                                                   ; OTHER INFORMATION: human ACS-1 antisense PCT-US03-25389-521
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OTHER INFORMATION: human ACS-1 antisense PCT-US03-25389-1106
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FCT-US03-25189-653/c
; Sequence 653, Application PC/TUS0325389
; GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 3624
SOFTWARE: Patentin version 3.2
SEQ ID NO 521
LENGTH: 20
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Matches 14; Conservative
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                                                                                                          ORGANISM: artificial FEATURE:
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                                                                                        TYPE: DNA
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Sequence 2031, Application PC/TUS0216840A

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Lev.
TITLE OF INVENTION: RAS, HERZ and HIV
FILE REFERENCE: 400/046 (MRHB02-326)
CURRENT PELLOGICHON NUMBER: PCT/US02/16840A
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US 60/236,249
PRIOR APPLICATION NUMBER: US 60/236,249
PRIOR PRILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 6810
SOFTWARE PATENTIN NUMBER: 300-05-29
NUMBER OF SEQ ID NOS: 6810
SOFTWARE PATENTIN VERSION 3.0
                                   TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Lev
TITLE OF INVENTION: RAS, HER2 and HIV
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Lev
TITLE OF INVENTION: RAS, HER2 and HIV
FILE REFERENCE: 400/046 (MBHB02-326)
CURRENT APPLICATION NUMBER: PCI/US02/16840A
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Best Local Similarity 88.2%; Pred. No. 4.8e+02;
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54.7%; Pred. No. 4.8e+02;
                                                    TITLE OF INVENTION: RAS, HERE and HIVE CURRENT APPLICATION RAS, HERE and HIVE FILE REFERENCE: 400/046 (MEHBO2-126)
CURRENT APPLICATION NUMBER: PCT/US02/16840
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US 60/318,471
PRIOR APPLICATION NUMBER: US 60/296,249
PRIOR PILING DATE: 2001-06-06
PRIOR PILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/294,140
PRIOR PILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 6810
SCFTWARE: PATENTIN PURSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LENGTH: 17
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Roswiggen, James
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
TITLE OF INVENTION: Ras, HER2 and HIV
FILE REPREBUCE: 400/046 (MBHB02-326)
CURRENT APPLICATION NUMBER: PCT/US02/16840
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US 60/316,471
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 6810
SOFTWARE: Patentin version 3.0
LENGTH: 17
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                                         APPLICANT: GOFF, STEPHEN
APPLICANT: GORNA, CAROLINE
APPLICANT: BONAN, CAROLINE
APPLICANT: BONAN, CAROLINE
APPLICANT: COLBERT, MICHELLE
APPLICANT: WANG, RONG-LIN MICHELLE
TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
TITLE REFRENCE: NADII. 1.05 8C1
CURRENT APPLICATION NUMBER: US 10/266,090
CURRENT FILING DATE: 2002-10-03
PRIOR PLICATION NUMBER: US 10/260,703
PRIOR APPLICATION NUMBER: US 60/326,117
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 51812
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 39932
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.6%; Score 14; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 5.2e+02; Matches 14; Conservative 0; Mismatches 0; Indels
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Pred. No. 4.8e+02;
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Sequence 39932, Application US/10266090 GENERAL INFORMATION:
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Best Local Similarity 64.77
Matches 11; Conservative
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Sequence 1266, Application US/09740332
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relative Or INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: RPI 400/003
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: Patentin version 3.0
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TITLE OF INVENTION: Method and Reagent for the Inhibition of ERG
FILE REFERENCE: 249/006
CURRENT APPLICATION UNBER: US/09/572,021
CURRENT FILING DATE: 2000-05-16
SOFTWARR: Patentin version 3.0
SEQ ID NO 2010
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88.2%; Pred. No. 4.8e+02;
iive 0; Mismatches 2; Indels
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88.2%; Pred. No. 4.8e+02;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Oligonucleotide substrate US-09-277-026B-6359
       CURRENT APPLICATION NUMBER: US/09/277,026B CURRENT FILING DATE: 1999-03-25 PRIOR APPLICATION NUMBER: US 60/079,678 PRIOR FILING DATE: 1998-03-27 NUMBER OF SEQ ID NOS: 6652 SOFTWARE: Patentin version 3.0 LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ribozyme Pharmaceuticals, Inc. APPLICANT: Jarvis, Thale
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; Sequence 2010, Application US/09572021
; GENERAL INFORMATION:
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Von Carlowitz, Ira
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                                                                                                                                                                                                   TYPE: RNA
ORGANISM: Artificial Sequence
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Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
LOCATION:
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 15; Conserv
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LENGTH: 17
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APPLICANT:
APPLICANT:
APPLICANT:
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1. Sequence 6359, Application US/09277026B

1. Sequence 6359, Application US/09277026B

2. Sequence 6359, Application US/09277026B

3. Sequence 6359, Application US/09277026B

4. PELICANT: Roberts, Elisabeth

3. APPLICANT: Coehott, Claire

4. APPLICANT: Coehott, Claire

4. APPLICANT: McSwiggen, James

5. APPLICANT: McSwiggen, James

5. TITLE OF INVENTION: Method and Reagents for the Treatment of Diseases or Conditions FITLE OF INVENTION: To Molecules Involved in Angiogenic Reponses

5. FILE REFERENCE: MBHB00-824-A (239/121)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ravoo, Pamela
APPLICANT: Roberts, Elisabeth
APPLICANT: Roberts, Elisabeth
APPLICANT: Abarvis, Thale
APPLICANT: Coeshott, Claire
APPLICANT: Coeshott, Claire
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Mcthod and Reagents for the Treatment of Diseases or Conditions F
TITLE OF INVENTION: to Molecules Involved in Angiogenic Reponses
FILE REFERENCE: MBHB00-824-A (239/121)
CURRENT APPLICATION WUMBRE: US/09/277,026B
CURRENT FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 60/079,678
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52.9%; Pred. No. 4.8e+02;
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US 60/318,471
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/294,140
PRIOR PLING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 6810
SOFTWARE: Patentin Version 3.0
SEQ ID NO 5019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6346, Application US/09277026B GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.0
SEQ ID NO 6346
LENGTH: 17
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CORGANISM: Homo sapiens
PCT-US02-16840A-5019
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Best Local Similarity
Matches 9; Conserv
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APPLICANT: Karpelsky, Alex
APPLICANT: Adamic, Jasenka Matulic
APPLICANT: Adamic, Jasenka Matulic
APPLICANT: Sweedler, Dave
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nuclectide Triphosphate and their Incorporation into Oligomucl,
FILE REFERENCE: MHSG00-83-F (400/009)
CURRENT PELING DATE: 1909-12-7
PRIOR APPLICATION NUMBER: 09/476,387
PRIOR PILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: 09/474,432
PRIOR APPLICATION NUMBER: 09/474,432
PRIOR PILING DATE: 1999-12-29
PRIOR PILING DATE: 1999-12-29
PRIOR PELING DATE: 1999-11-04
PRIOR PELING DATE: 1998-10-04
PRIOR PELING DATE: 1998-04-29
PRIOR PELING DATE: 1998-04-29
PRIOR PELING DATE: 1999-12-05
PRIOR PELING DATE: 1998-04-29
PRIOR PELING DATE: 1999-12-05
PRIOR PELING DATE: 1998-04-29
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APPLICANT: Lawrence Blatt
APPLICANT: James McSwiggen
APPLICANT: James McSwiggen
APPLICANT: Bharat Chowrins
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Recepto
FILE REFERENCE: MBHB00-878-C (400/017)
CURRENT APPLICATION NUMBER: 09/780,533
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 2617
SOFTWARE: Patentin version 3.0
SEQ ID NO 328
LENGTH: 17
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88.2%; Pred. No. 4.8e+02;
tive 0; Mismatches 2;
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; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
                                                                                                                                                                                  APPLICANT: Ribozyme Pharmaceuticals, Inc
                                                                                                                      ; Sequence 676, Application US/09825805; GENERAL INFORMATION:
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Best Local Similarity 88.2
Matches 15; Conservative
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Beaudry, Amber
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REPERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: PatentIn version 3.0
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APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
CURRENT APPLICATION NUMBER: US/09/780,164
CURRENT APPLICATION NUMBER: 201-02-09
PRIOR APPLICATION NUMBER: 60/185,516
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 2603
SOFTWARE: Patentin version 3.0
SEQ ID NO 840
LENGTH: 17
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                                                                                                                                               Query Match 0.6%; Score 13.8; DB 1; Length 17; Best Local Similarity 82.4%; Pred. No. 4.8e+02; Matches 14; Conservative 1; Mismatches 2; Indels
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Best Local Similarity 82.4%; Pred. No. 4.8e+02;
Matches 14; Conservative 1; Mismatches 2;
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                                                         OTHER INFORMATION: oligonucleotide substrate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ribozyme Pharmaceuticals, Inc. APPLICANT: Blatt, Larry APPLICANT: McSwiggen, Jim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 840, Application US/09780164 GENERAL INFORMATION:
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NAME/KEY: misc_feature
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Best Local Similarity
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                                                                                         US-09-740-332-1266
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LENGTH: 17
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GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Daper, Ken
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Reli
TITLE OF INVENTION: Levels of NF-Kappa B
FILE REFERENCE: 400/022 (MBHB00-812-D)
CURRENT APPLICATION NUMBER: US/09/864,785
CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 3929
SOUTHARE: Patentin version 3.0
SEQ ID NO 583
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APPLICANT: Blatt, Lavrence
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Nucleir Acid-Based Treatment of Diseases or Conditions Related
TITLE OF INVENTION: Nile Virus Infection
FILE REFERENCE: MBHB00,1109-A (400/037)
CURRENT APPLICATION NUMBER: US/10/017,974
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 37080
SOFTWARE: Patentin version 3.0
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US-09-864-785-583
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                                                                                                                                                                                                                                                                                                                 2; Indels
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         CURRENT APPLICATION NUMBER: US/09/863,041A
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; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
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                      CURRENT FILING DATE: 2001-05-22
NUMBER OF SEQ ID NOS: 3929
SCFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 583
LENGTH: 17
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ORGANISM: Artificial Sequence
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US-10-017-974-8720
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Best Local Similarity
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US-09-864-785-583
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                                                                                                                                                                                                                                                        APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate TITLE OF INVENTION: Levels of Enjdermal Growth Factor Receptors
FILE REPERBNCE: MBHB00-958-I (400/018)
CURRENT APPLICATION NUMBER: US/09/848,754A
CURRENT PILLIG DATE: 2001-05-03
NUMBER OF SEO ID NOS: 9645
SOFTWARE: Patentin version 3.0
SEO ID NO 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2182, Application US/09848754A
Sequence 2182, Application US/09848754A
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
TITLE NBHORDS MARBOO-958-I (400/018)
CURRENT APPLICATION NUMBER: US/09/848,754A
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 9645
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APPLICANT: Draper, Ken
APPLICANT: Draper, Ken
APPLICANT: McSwiggen, Jim
IITLE OF INVENTION: Levels of NF-Kappa B
FILE REFERENCE: 400/022 (MBHB00-812-D)
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88.2%; Pred. No. 4.8e+02;
tive 0; Mismatches 2; Indels
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88.2%; Pred. No. 4.8e+02;
tive 0; Mismatches 2
                      Mismatches
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Stinchoomb, Dan
  76.5%; Pred. No.
                                                                                                                                                                                                              Sequence 61, Application US/09848754A GENERAL INFORMATION:
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                      13; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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US-09-848-754A-2182
Best Local Similarity
                                                                                                                                                                       RESULT 752
US-09-848-754A-61/c
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SEQ ID NO 2182
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICATW: ROSettadenomics
TITLE OF INVENTION: BLOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
FILE REFERENCE: 47416
CURRENT APPLICATION NUMBER: 20/2-11-26
NUMBER OF SEQ ID NOS: 17608
SOFTWARE: PARENTING DATE: 2002-11-26
SOFTWARE: PARENTING DATE: 2002-11-36
SOFTWARE: PARENTING DATE: 2003-11-36
SOFTWARE: PARENTING DATE: 2003-11-36
SOFTWARE: PARENTING DATE: 2003-11-36
SOFTWARE: PARENTING DATE: 2003-11-36
SEQ ID NO 3691
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TITLE OF INVENTION: Escherichia coli O157:H7:EDL933, complete genome.
FILE REFERENCE: Jim Zegeer. 1037:684-8333
CURRENT APPLICATION NUMBER: LW/IO/294,037A
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 2772
SOFFWARE: Proprietary
SEQ ID NO 1194
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Pred. No. 4.8e+02;
0; Mismatches 2; Indels
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; LOCATION: (1711581) ... (1711596)

; OTHER INFORMATION: Chromosome = 1 Strand = positive

US-10-294-0374-1194
                   CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: PCT/US 02/16840
PRIOR FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 4666
SOFTWARE: Patentin version 3.0
SEQ ID NO 3352
             CURRENT APPLICATION NUMBER: US/10/238,700
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Matches 15; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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US-10-238-700-3352
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; ORGANISM: Homo sapiens
US-10-303-778-3691
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Best Local Similarity
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US-10-303-778-3691
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US-10-165-552-364/c
Sequence 364, Application US/10163552
Sequence 364, Application US/10163552
Sequence 364, Application US/10163552
Sequence Application Sequence Sequence
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TIPLEONT: McSwiggen, James
TIPLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
FILE REFERENCE: 400/057 (MBHB01-1158-A)
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88.2%; Pred. No. 4.8e+02;
live 0; Mismatches 2; Indels
      Length 17;
                                                                  Indels
                                                                                                                                                                                                                                                                                                              US-10-156-306-5078/c

| Sequence 5078, Application US/10156306
| GENERAL INFORMATION:
| APPLICANT: Ribozyme Pharmaceuticals, Inc.
| APPLICANT: Ribozyme Pharmaceuticals, Inc.
| TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment;
| TITLE OF INVENTION: Levels of IKK-Gamma and PKR;
| FILE REFERENCE: MBHB01-664-A (400/050)
| CURRENT APPLICATION NUMBER: US/10/156,306
| CURRENT FILING DATE: 2002-05-28
| NUMBER OF SEQ ID NOS: 8013
| SOFTWARE: PatentIn version 3.0
Score 13.8; DB 1;
Pred. No. 4.8e+02;
0; Mismatches 2;
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Matches 15; Conservative
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Matches 15; Conserv
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Matches 15; Conser
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LENGTH: 17
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Sequence 7281, Application US/10310188
Sequence 7281, Application US/10310188
SETEMENT INFORMATION:
APPLICANT: ROSEttaGemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY:
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT PILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SSO ID NO 72831
LEMGTH: 17
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TITLE OF INVENTION: Escherichia coli 0157:H7, complete genome.
FILE REPERENCE: Jim Zeger. Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/316,954
NUMBER OF SEQ ID NOS: 5998
SOFTWARE: Proprietary
SEQ ID NO 1929
                                                                                                   Score 13.8; DB 1; Length 17; Pred. No. 4.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 17;
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                                                                                                                                               Indels
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88.2%; Pred. No. 4.8e+02;
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88.2%; Pred. No. 4.8e+02;
ative 0; Mismatches 2;
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; Sequence 1929, Application US/10316954
; GENERAL INFORMATION:
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US-10-430-882-328
; Sequence 328, Application US/10430882
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OTHER INFORMATION: Chromosome = 1
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Best Local Similarity 88.2
Matches 15; Conservative
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                 ; TYPE: DNA
; CRGANISM: Homo sapiens
US-10-310-188-72805
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Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
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US-10-310-188-72831
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LENGTH: 17
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                                                                                                                                                                                      APPLICANT: Rosettagemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 864841
SOFTWARE: Patentin version 3.1
SEQ ID NO 5982
LENGTH: 17
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 4/487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
LENGHI. 17
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CURRENT APPLICATION NUMBER: US/10/310,188

CURRENT FILING DATE: 2002-12-19

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 72805
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Pred. No. 4.8e+02;
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Pred. No. 4.8e+02;
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S.10-310-189-72805/c
; Sequence 72805, Application US/10310188
; GENERAL INFORMATION:
                                                                                                                                                   Sequence 5982, Application US/10310188 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7330, Application US/10310188 GENERAL INFORMATION:
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          1251 CCCCATCCCCAACCCCC 1267
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Best Local Similarity 88.2%;
Matches 15; Conservative
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Best Local Similarity 88.2%;
Matches 15; Conservative
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US-10-310-188-5982
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 763
US-10-310-188-7330/c
                                                                                                          RESULT 762
US-10-310-188-5982
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APPLICANT: Blatt, Lawrence
APPLICANT: Blatt, Lawrence
APPLICANT: Blatt, Deter
APPLICANT: Chowrira, Bharat
APPLICANT: Habebril, Peter
APPLICANT: Habebril, Peter
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Fosnaugh, Kathy
ITILE OF INVENTION: Mcdulation of Gene Expression Associated with Inflammation Pro:
ITILE OF INVENTION: and Neurite Growth Using Nucleic Acid Based Technologies
ITILE REFERENCE: MBHB 02-258-PCT (400/045)
CURRENT APPLICATION NUMBER: US/10/471,271
CURRENT APPLICATION NUMBER: 60/181,797
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: 60/294,412
PRIOR PILING DATE: 2001-05-29
PRIOR PILING DATE: 2001-05-28
NUMBER OF SEQ ID NOS: 13274
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APPLICANT: Reneth, Roberts
TILLE OF INVENTION: OLIGONUCLECTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND H
TITLE OF INVENTION: VIRUS REPLICATION
TITLE OF INVENTION: VIRUS REPLICATION
FILE REPERENCE: 400/042US (MEHBO2-249-E)
CURRENT APPLICATION NUMBER: US/10/669,841
CURRENT PILING DATE: 2003-09-23
FRIOR PILING DATE: 2000-06-66
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR APPLICATION NUMBER: US 60/335,059
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US 60/335,059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid US-10-471-271-1547
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                                                                                                                                                                                                                 ; Sequence 1547, Application US/10471271; GENERAL INFORMATION:
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APPLICANT: Lawrence, Blatt
APPLICANT: Dennis, Macejak
   1045 ACTAAGCCCCTGGCCCC 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1204 CCCTATCAGGGGGCTGA 1220
                                   1 ACUGAGGCCCUGGCCCC 17
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ORGANISM: Artificial Sequence
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David, Morrissey
                                                                                                                                                      RESULT 769
US-10-471-271-1547/c
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LENGTH: 17
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APPLICANT:
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APPLICANT: Chowrira, Bharat

APPLICANT: Chowrira, Bharat

APPLICANT: Chowrira, Bharat

APPLICANT: Hacberili, Peter

APPLICANT: Hacberili, Peter

APPLICANT: McSwiggen, James

APPLICANT: Fosnaugh, Kathy

ITITLE OF INVEXTION: Modification of Gene Expression Associated with Inflammation Prolif

ITITLE OF INVEXTION: Modification of Gene Expression Associated with Inflammation Prolif

ITITLE OF INVEXTION: Modification of Gene Expression Associated with Inflammation Prolif

ITITLE OF INVEXTION NUMBER: US/10/471,271

CURRENT APPLICATION NUMBER: 60/181,797

PRIOR FILING DATE: 2000-02-01

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-08-05

NUMBER OF SEQ ID NOS: 13274

SOFURDARE: Patentin version 3.0

SEQ ID NO 328
         APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Lawrence Blatt
APPLICANT: Lawrence Blatt
APPLICANT: Lawrence Blatt
APPLICANT: Dames McSwigen
APPLICANT: Bharat Chowrina
APPLICANT: Bharat Chowrina
APPLICANT: Bharat Chowrina
APPLICANT: Peter Haeberli
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
FILE REFERENCE: MBHB00-878-H (400/112)
CURRENT APPLICATION NUMBER: US/10/430,882
CURRENT APPLICATION NUMBER: 09/82/33
PRIOR APPLICATION NUMBER: 09/780,533
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2002-04-03
NUMBER: PCT/US02/10512
PRIOR FILING DATE: 2002-04-03
NUMBER: PAGENT NUMBER: PCT/US02/10512
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 2617
SEQ ID NO 328
LENGTH: 17
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0.6%; Score 13.8; DB 1; Length 17;

Best Local Similarity 76.5%; Pred. No. 4.8e+02;

Matches 13; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 4.8e+02;
Matches 13; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 328, Application US/10471271 GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-10-430-882-328
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ORGANISM: Homo sapiens
GENERAL INFORMATION:
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APPLICANT: SHANNOW, MARK

TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART
FILE REPERENCE: PB0105
CURRENT APPLICATION NUMBER: US/10/723,361
CURRENT PILING DATE: 2003-11-26
PRIOR PELING DATE: 2000-05-25
PRIOR PELING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-04
PRIOR PILING DATE: 2001-01-04
PRIOR PILING DATE: 2001-01-07
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
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TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART
FILE REPERENCE: PB0105
CURRENT APPLICATION NUMBER: US/10/723,361
CURRENT FILING DATE: 2003-11-26
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88.2%; Pred. No. 4.8e+02;
live 0; Mismatches 2;
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PRIOR APPLICATION NUMBER: US 09/866,108

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PELICATION NUMBER: US 60/203.6

PRIOR FILING DATE: 2000-00-4

PRIOR FILING DATE: 2000-00-4

PRIOR FILING DATE: 2000-00-67

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
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Best Local Similarity
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APPLICANT:
APPLICANT:
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GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
TITLE OF INVENTION: USES THEREOF
FILE REFERRNCE: 49992
CURRENT FAPLICATION NUMBER: US/10/707,147
CURRENT FALLNG DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 20189
SOFTWARE: Patentin version 3.2
SEQ ID NO 5148
LENGTH: 17
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                         PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR FILING DATE: 2002-03-124
PRIOR FILING DATE: 2002-03-11
PRIOR PLING DATE: 2002-03-11
PRIOR PLING DATE: 2002-03-11
PRIOR PLING DATE: 2001-03-26
PRIOR PLING DATE: 2000-13-26
PRIOR PLING DATE: 2000-12-18
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: US 09/504,321
PRIOR PLING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: US 09/504,321
PRIOR PLING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/504,321
PRIOR APPLICATION NUMBER: US 09/504,331
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OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
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Pred. No. 4.8e+02;
0; Mismatches 2;
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FILING DATE: 2001-12-05
APPLICATION NUMBER: US 60/358,580
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GENERAL INFORMATION:
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Best Local Similarity 88.2%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David K.
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LOCATION:
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US-10-707-147-5148
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APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Miswiggen, James
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Lev
TITLE OF INVENTION: RAS, HERZ and HIV
FILE REFERENCE: 400/046-US (MBHB02-326-A)
CURRENT PELLING DATE: 2003-01-26
PRIOR PELLING DATE: 2003-01-26
PRIOR PELLING DATE: 2001-09-10
PRIOR PELLING DATE: 2001-06-06
PRIOR PELLING DATE: 2001-06-06
PRIOR PELLING DATE: 2002-09-10
PRIOR PELLING DATE: 2002-09-06
PRIOR PELLING DATE: 2002-09-10
PRIOR PELLING DATE: 2002-09-06
PRIOR PELLING DATE: 2003-05-29
PRIOR PELLING DATE: 2003-05-23
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| Sequence 20, Application PC/TUS0337416
| GENERAL INFORMATION:
| APPLICANT: Scios, Inc.
| APPLICANT: Feng, Ying
| APPLICANT: Feng, Ying
| APPLICANT: Higgings, Linda
| APPLICANT: Engoun, Ann
| APPLICANT: Colvent George
| TITLE OF INVENTION: METHOD FOR COUNTERACTING A PATHOLOGIC
| TITLE OF INVENTION: CHANGE IN THE BETA-ADRENERGIC PATHWAY
| TITLE OF INVENTION: CHANGE IN THE BETA-ADRENERGIC PATHWAY
| TITLE OF INVENTION: CHANGE IN THE BETA-ADRENERGIC PATHWAY
| TITLE OF INVENTION: CHANGE IN THE BETA-ADRENERGIC PATHWAY
| TITLE OF INVENTION NUMBER: E0/504585
| PRIOR APPLICATION NUMBER: 60/504585
| PRIOR PLING DATE: 2003-09-18
| PRIOR PLING DATE: 2003-09-18
| PRIOR PLING DATE: 2003-09-18
| PRIOR PLING DATE: 2003-01-22
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88.2%; Pred. No. 4.8e+02;
tive 0; Mismatches 2; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LEMOTH: 18
                            US-10-724-270-5019/c; Sequence 5019, Application US/10724270; GENERAL INFORMATION:
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Best Local Similarity 88.2

--her 15; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
TITLE OF INVENTION: Nas, HER2 and HIV
FILE REFERENCE: 400/046-US (MBHB02-326-A)
CURRENT FILING DATE: 2003-11-26
PRIOR PELICATION NUMBER: US 60/236,249
PRIOR PLING DATE: 2001-06-06
PRIOR PLING DATE: 2001-06-06
PRIOR PLING DATE: 2001-06-06
PRIOR PLING DATE: 2002-06-06
PRIOR PLING DATE: 2003-06-29
PRIOR PLING DATE: 2003-06-29
PRIOR PLING DATE: 2003-06-29
PRIOR PLING DATE: 2003-06-26
PRIOR PLING DATE: 2003-06-29
PRIOR PLING DATE: 2003-06-29
PRIOR PLING DATE: 2003-06-20
PRIOR PRIOR PLING DATE: 2003-06-20
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SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                         See File Wrapper or PALM.
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0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See Number OF SKO ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2031, Application US/10724270 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.054 CTGGCCCCCAAACCCAAG 1070
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US-10-724-270-2031
                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-723-361-972
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Best Local Similarity
Matches 11, Conserv
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                                                                                                                                                                                                                                                                                                                  SEQ ID NO 972
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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RESULT 779
US-08-170-096-5
US-08-170-096-5

US-08-170-096-5

SEQUENCE 5, Application US/08170096

GENERAL INFORMATION:
APPLICANT: Dixon, Larry A.
APPLICANT: Rege, Ajay A.
APPLICANT: Dixon, Richard A.F.
ITILE OF INVENTION: PIRROBLAST GROWTH FACTOR RECEPTOR GENE FAMILY NUMBER OF SEQUENCES: 29
CORRESPONDENCE 2DESSLE: Ajlamanow, Ltd.
ADDRESSEE: Milnamow, Ltd.
STREET: 180 North Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                                                                                                   Sequence 5, Application US/07999706
GENERAL INFORMATION:
APPLICANT: Denner, Larry A.
APPLICANT: Denner, Larry A.
APPLICANT: Dixon, Richard A.F.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR RECEPTOR GENE NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Milnamow, Ltd.
STREET: 180 North Stetson, Suite 4700
CITY: Chicago
STREET: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·.
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SOFTWARE: PATORILIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/999,706
FILING DATE: 19921231
CLASSIFICATION: 435
ATTONENY/AGENT INFORMATION:
NAME: RALL MARTIN LIN.
REGISTRATION NUMBER: 25,011
TELEPHONE: (312)616-5400
TELEPAX: (312)616-5400
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TTYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
TYPE: ACID
TYP
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Floppy
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Best Local Similarity
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; MOLECULE TYPE:
US-07-999-706-5
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                                                                                                       S-907-999-706-5
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                                                                                                                                                  Query Match 0.6%; Score 13.8; DB 1; Length 18; Best Local Similarity 88.2%; Pred. No. 5.1e+02; Matches 15; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 67, Application PC/TUS9600162A
GENERAL INFORMATION:
APPLICANT: Yang, O'OUNG
APPLICANT: Yang, O'OUNG
APPLICANT: Cereb, Nezih
TITLE OF INVENTION: Methods and Reagents for Typing HLA
TITLE OF INVENTION: Class I Genes
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson
STREET: 1992 Commerce Street Suite 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Diskette - 3.5 inch, 1.44 Mb storage
IBM compatible
SYSTEM: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSK.P-001-US
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00362A
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                                                                                                                                                                                                                                                                         1134 CACCTCCAGCTCCACCT 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: LATSON, MATINA T. REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: MSK
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (914) 245-3252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      731 AGGAGAAACAGAACACC 747
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (914) 962-4330 TELEX:
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Best Local Similarity 88.2°
Matches 15; Conservative
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                                                        OTHER INFORMATION: primer
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM CON OPERATING SYSTEM:
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FRAGMENT TYPE: i
ORIGINAL SOURCE:
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OTHER INFORMATION: hybridization probe GE2-183 for typing of HLA Class I gene
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US-09-668-558A-94/C

Sequence 94, Application US/09668558A

GENERAL INFORMATION:
APPLICANT: Frances
APPLICANT: Erickson, Mary Ruth
APPLICANT: Binain, Bernard
TILLE OF INVENTION: LSR-Leptin Interaction and Their Use in the Prevention
TILLE OF INVENTION: and Treatment of Obesity-Related Diseases
TILLE REPERENCE: 70.US2.REG
CURRENT APPLICATION NUMBER: US/09/668,558A
CURRENT FILING DATE: 2001-03-12
PRIOR PILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 106
SEQ ID NO 94
LENGTH: 18
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GENERAL INFORMATION:
APPLICANT: Yen, Frances
APPLICANT: Exiden, Mary Ruth
APPLICANT: Exiden, Mary Ruth
APPLICANT: Binain, Bernard
ITILE OF INVENTION: LSR-Leptin Interaction and Their Use in the Prevention
ITILE OF INVENTION: LSR-Leptin Interaction and Their Use in the Prevention
ITILE OF INVENTION: and Treatment of Obesity-Related Diseases
CURRENT APPLICATION NUMBER: US/09/668,558B
CURRENT FILING DAIE: 200-09-22
CURRENT FILING DAIE: 1999-09-22
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                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                          Query Match 0.6%; Score 13.8; DB 1;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.6%; Score 13.8; DB 1; Best Local Similarity 88.2%; Pred. No. 5.1e+02; Matches 15; Conservative 0; Mismatches 2;
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOMECULE TYPE: other nucleic acid
HYPOTHETICAL: no
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ORGANISM: Artificial Sequence
                                                                                                                              internal
                                                                                                        ANTI-SENSE: yes
FRAGMENT TYPE: inte
ORIGINAL SOURCE:
ORGANISM: human
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0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yang, Soo Young
APPLICANT: Cereb, Nezih
TITLE OF INVENTION: Methods and Reagents for Typing HLA
TITLE OF INVENTION: Class I Genes
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson LLP
STREET: P.O. Box 5270
CITY: Frisco
             CONTER: US
ZIP: 80443
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Perfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Larson, Marina T.
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: MSK.P-001-DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 668-2082
TELEFAX: (970) 668-2082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/342,375
    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION DATA:
FILING DATE: December 22, 1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1134 CACCTCCAGCTCCACCT 1150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
US-08-170-096-5
                                                                                                                                                                                                                                                                                                                  TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA US-10-266-090-50685
                                                                                                                                                                                                                                                                                                               Sequence 50665, Application US/10266090
; GENERAL INPORMATION:
; APPLICANT: GOFF, STEPHEN
; APPLICANT: GOFF, STEPHEN
; APPLICANT: COLENET, MICHELLE
; APPLICANT: WANG, RONG-LIN
; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
; TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
; TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
; TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
; TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
; TILE REFERENCE: NADII.058C1
; CURRENT APPLICATION NUMBER: US 10/266,090
; CURRENT FILING DATE: 2002-10-03
; PRIOR FILING DATE: 2002-02-66
; PRIOR PLING DATE: 2001-09-26
; SOFTWARE: PESESCE FOR WINDOWS VERSION 4.0
; SEQ ID NO 50685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 18;
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APPLICANT: BOLAN, CAROLINE

APPLICANT: COLBERT, MICHELLE

APPLICANT: COLBERT, MICHELLE

APPLICANT: COLBERT, MICHELLE

APPLICANT: WANG, RONG-LIN

TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE

TITLE OF INVENTION: CEREAL MARKERS AND THEIR USES

FILE REFERENCE: NADII.058C1

CURRENT PELLING DATE: 2002-10-03

CURRENT FILING DATE: 2002-10-03

FRIOR FILING DATE: 2002-09-26

PRIOR FILING DATE: 2001-09-26

NUMBER OF SEQ ID NOS: 51812

SOFTWARE: FASISEQ for Windows Version 4.0

SEQ ID NO 50690
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                                Indels
Best Local Similarity 88.2%; Pred. No. 5.1e+02; Matches 15; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

0.6%; Score 13.8; DB 1;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 13.8; DB 1;
Pred. No. 5.1e+02;
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GENERAL INFORMATION:
APPLICANT: GOPF, STEPHEN
APPLICANT: GOLBERT, MICHELLE
APPLICANT: WANG, RONG-LIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1134 CACCTCCAGCTCCACCT 1150
                                                                                                       912 CTTTGGTCTTTGCCTTT 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 caccaccaccicacci
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Best Local Similarity
                                                                                                                                                                                                                                                                    RESULT 785
US-10-266-090-50685/c
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                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                       ; OTHER INFORMATION: oligonucleotide Zinc finger nuclotides of SEQID1 US-09-668-5588-94
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1S-09-969-373-4117/c

1S-09-969-373-4117/c

SEQUENCE 1INFORMATION:

SECRETAL INFORMATION:

APPLICANT: Effertz, Roger J.

APPLICANT: Hauge, Brian M.

TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping

TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping

CURRENT APPLICATION NUMBER: US/09/969,373

CURRENT APPLICATION NUMBER: US 09/754,853

PRIOR FILING DATE: 2001-01-05

PRIOR FILING DATE: 2001-01-05

PRIOR FILING DATE: 2001-01-03

PRIOR FILING DATE: 2001-01-03

PRIOR FILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 4593

SEQ ID NO 4117
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                                                                                                                                                                                                                                                                                                                                        Query Match
0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11arity 88.2%; Pred. No. 5.1e+02; Conservative 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14873, Application US/09703708 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Xanthomonas campestris US-09-703-708-14873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1235 CAGCCCTCGCCTCCGAC 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 CAGCCCTCGGCTCCCAC 1
                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      964 CAACGGTGGAAGTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 chargergangeccha
   NUMBER OF SEQ ID NOS: 106
SOFTWARE: Patent.pm
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-703-708-14873
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                                                                       SEQ ID NO 94
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                                                                                                                                                                                                              FEATURE:
                                                                                                              LENGTH:
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Sequence 21226, Application US/10310188
GENERAL INFORMATION:
APPLICANT: RosettaGemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G.
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION UNDER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
SOFTWARE: PATENTIN VOS: 86841
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10552, Application US/10310188
GENERAL INFORMATION:
APPLICANT: RosettaGemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF EXPLICANTION WIMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE PARENTIN VERSION 3.1
SEQ ID NO 10552
LENGTH: 18
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0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                        Length 18;
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                                                                                                                                 Query Match
0.6%; Score 13.8; DB 1;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2;
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9.10-310-1188-24811/c
; Sequence 24811, Application US/10310188
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                    1127 CCACCTTCACCTCCAGC 1143
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CONGANISM: Homo sapiens
US-10-310-188-21226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                      LENGTH: 18
TYPE: DNA
CRGANISM: Homo sapiens
US-10-310-188-9756
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US-10-310-188-10552/c
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US-10-310-188-21226
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LENGTH: 18
SEQ ID NO 9756
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GENERAL INFORMATION:
APPLICANT: ROSettadementics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT PILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86641
SOFTWARE: Patentin version 3.1
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US-10-310-188-6215

Sequence 6215, Application US/10310188

GENERAL INFORMATION:
APPLICANT: ROSettademonics
TITLE OF INVENTION: USES THEREOF
TITLE OF UNENTION: USES THEREOF
THEREOF SEQUENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PATENTIN VERSION 3.1
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    Gaps
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
TITLE OF INVENTION: BEGINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
FILE REFERENCE: 47416
CURRENT APPLICATION NUMBER: US/10/303,778
CURRENT FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 17608
SOFTWARE: PATENTING DATE: 2002-11-25
LENGTH: 18
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  Indels
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88.2%; Pred. No. 5.1e+02;
iive 0; Mismatches 2;
  Mismatches
                                                                                                                                                                                                            Sequence 5025, Application US/10303778 GENERAL INFORMATION:
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                                                 1134 CACCTCCAGCTCCACCT 1150
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    Conservative
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US-10-310-188-6215
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Best Local Similarity
Matches 15; Conserv
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US-10-303-778-5025/c_
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LENGTH: 18
    15;
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    Matches
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: RosettaGemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENTILE OF INVENTION: USES THEREOF;
TILE REFERENCE: 47487
FILE REFERENCE: 47487
CURRENT APPLICATION UNMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SEQ ID NOS: 86841
SEQ ID NO 35499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-188-39123/c
US-10-188-39123, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: ROSELtaGemennics
; TITLE OF INVERTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GE:
; TITLE OF INVERTION: USES THEREOF
; TITLE OF INVERTION: USES THEREOF
; TITLE OF INVERTION: USES THEREOF
; CURRENT APPLICATION VMBER: US/10/310,188
; CURRENT APPLICATION VMBER: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 39123
; TYPE: DNA
                                                                                                                                                                 TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENTITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENTITLE OF INVENTION: USES THEREOF FILE REPRENCE: 47487 CURRENT APPLICATION NUMBER: US/10/310,188 CURRENT PILING DATE: 2002-12-19 NUMBER OF SEQ ID NOS: 86841 SEQ ID NOS: 86841 SEQ ID NOS: 86841 SEQ ID NO 34820 LENGTH: 18
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Pred. No. 5.1e+02;
0; Mismatches 2; Indels
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Pred. No. 5.1e+02;
0; Mismatches 2;
                                                                                                                                Sequence 34820, Application US/10310188 GENERAL INFORMATION:
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17 TGGACACCTGACAAGA
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Best Local Similarity 86.4.
Best Local Si Conservative
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Best Local Similarity 88.29
Matches 15; Conservative
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CRGANISM: Homo sapiens
US-10-310-188-34820
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US-10-310-188-35499
                                                                                     RESULT 795
US-10-310-188-34820/c
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US-10-310-188-35499
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US-10-188-25793

US-10-188-25793

Sequence 25793, Application US/10310188

Sequence 25793, Application US/10310188

SEQUENCE TIVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENERAL TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: 4746

CURRENT APPLICATION NUMBER: US/10/310,188

CURRENT FILING DATE: 2002-12-19

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 25793

LENGTH: 18
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APPLICANT: ROSettaGemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: UNDER: US/10/310,188
CURRENT APPLICATION UNDER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOGTWARE: Patentin version 3.1
SEQ ID NO 30755
LENGTH: 18
APPLICANT: RosettaGemonics
TITLE OF INVENTION: BIOINPORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION WINDBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 48811
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                    Query Match 0.6%; Score 13.8; DB 1; Length 18; Best Local Similarity 88.2%; Pred. No. 5.1e+02; Matches 15; Conservative 0; Mismatches 2; Indels
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0.6%; Score 13.8; DB 1; Length 1
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
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US-10-310-188-24811
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Best Local Similarity
Matches 15; Conserva
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US-10-310-188-30755/c
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APPLICANT: ROSELTEGEMONICS
APPLICANT: ROSELTEGEMONICS
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GE
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: UNBER: US/10/310,188
CURRENT APPLICATION UNBER: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 72795
LENGTH: 18
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APPLICANT: RosettaGemonics .

TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487

CURRENT APPLICATION NUMBER: 12/0/310,188

CURRENT FILING DATE: 2002-12-19

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: Patentin version 3.1

SEQ ID NO 72796

LENGTH: 18
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88.2%; Pred. No. 5.1e+02;
tive 0; Mismatches 2;
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ilarity 88.2%; Pred. No. 5.1e+02;
Conservative 0; Mismatchor
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88.2%; Pred. No. 5.1e+02;
tive 0; Mismatches 2;
FILE REFERENCE: 47487
CURRENT PEPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 72778
LENGTH: 18
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Best Local Similarity 88.2
Matches 15, Conservative
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US-10-310-188-72796
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US-10-310-188-72795
                                                                                                                                               CRGANISM: Homo sapiens
US-10-310-188-72778
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Matches 15; Conserv
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                  TYPE: DNA
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; Sequence 72778, Application US/10310188
; GENERAL INFORMATION:
; TIPLE CMT: ROSELTAGEmonics
; TIPLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; TIPLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                           APPLICANT: ROSETTEGEMONICS
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SEQ ID NO 55156
LENGTH: 18
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Pred. No. 5.1e+02;
0; Mismatches 2; Indels
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                                                     Score 13.8; DB 1; Length 18;
Pred. No. 5.1e+02;
0; Mismatches 2; Indels
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Pred. No. 5.1e+02;
0; Mismatches 2;
                                                                                                                                                                                                                            RESULT 798
Vs.10-310-188-55156
Sequence 55156, Application US/10310188
GENERAL INFORMATION
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Best Local Similarity 88.2%;
Matches 15; Conservative
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Best Local Similarity 88.2'
Matches 15; Conservative
                                                               Query Match
Best Local Similarity 88.23
Matches 15; Conservative
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CRGANISM: Homo sapiens
US-10-310-188-60065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-55156
         ; ORGANISM: Homo sapiens
US-10-310-188-39123
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Sequence 14873, Application US/60183791
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bower, Stanley G.
TITLE OF INVENTION: Xanthemonas campestris Genome Sequences and Uses Thereof
TITLE OF INVENTION: Xanthemonas campestris Genome Sequences and Uses Thereof
TITLE REFERENCE: 38-10(15804)B
CURRENT APPLICATION NUMBER: US/60/183,791
CURRENT FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 18992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bower, Stanley G.
APPLICANT: Bower, Gregory J.
TITLE OF INVENTION: Xanthomonas campestris Genome Sequences and Uses Thereof
FILE REPERENCE: 38-10(15804)A
CURRENT APPLICATION NUMBER: US/60/164,320
CURRENT FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 18992
SEQ ID NO 14873
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                                                                                                                                                                                                   Length 18;
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                                                                                                                                                                                                     Score 13.8; DB 1;
Pred. No. 5.1e+02;
                                                                                                                                                                                                                                              0; Mismatches
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
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Second 44873
Second 14873, Application US/60164320
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Xanthomonas campestris
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                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 88.2%;
Matches 15; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                            ; OTHER INFORMATION: primer US-10-718-948-20
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Best Local Similarity
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US-60-183-791-14873
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LENGTH: 18
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US-10-321-039-630
                   SOFTWARE: Fat
SEQ ID NO 20
LENGTH: 18
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                                                                                                                           FEATURE:
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SEQ ID NO 85927
LENGTH: 18
                                                                                                     APPLICANT: RosettaGemonics
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION UNMERE: US/10/310,188
CURRENT APPLICATION UNMERE: 202-12-19
NUMBER OF SEQ ID NOS: 86841
SECTION OF SEQ ID NOS: 86841
SECTION OF SEQ ID NOS: 86841
SEQ ID NOS: 82799
LENGTH: 18
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Pred. No. 5.1e+02;
0; Mismatches 2; Indels
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APPLICANT: Liu, David
APPLICANT: Liu, David
APPLICANT: Schreiner, George
TITLE OF INVENTION: METHOD FOR COUNTERACTING A PATHOLOGIC
TITLE OF INVENTION: CHANGE IN THE BETA-ADRENERGIC PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 39739-0029
CURRENY APPLICATION NUMBER: US/10/718,948
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/504585
PRIOR PILING DATE: 2003-09-18
PRIOR PILING DATE: 2003-09-18
PRIOR PILING DATE: 2002-11-22
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80.10-310-188-85927/c
Sequence 85927, Application US/10310188
GENERAL INFORMATION:
                                                                 Sequence 72799, Application US/10310188 GENERAL INFORMATION:
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APPLICANT: Higgings, Linda
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US-10-310-188-85927
                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-10-310-188-72799
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Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
Matches 15; Conserv
                                             US-10-310-188-72799/c
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GENERAL INFORMATION:
EAPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Peeudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 64158
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88.2%; Pred. No. 5.3e+02;
ive 0; Mismatches 2; Indels
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
FEATURE:
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88.2%; Pred. No. 5.3e+02;
tive 0; Mismatches 2;
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APPLICANT: Russell, Deanna L.
APPLICANT: Russell, Deanna L.
APPLICANT: Battuck, Donna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: DIABETES GENE
FILE REFERENCE: Diabetes Gene III
CURRENT APPLICATION NUMBER: PCT/US00/13327
CURRENT FILING DATE: 2000-05-16
PRIOR FILING DATE: 2000-01-06
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 48
LENGTH: 19
FILE REFERENCE: Diabetes Gene III
CURRENT APPLICATION NUMBER: PCT/US00/13327
CURRENT FILING DATE: 2000-05-16
PRIOR APPLICATION NUMBER: US 60/174,700
PRIOR FILING DATE: 2000-01-06
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 88.2
Matches 15; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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; ORGANISM: Homo sapiens
PCT-US00-13327-46
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SEQ ID NO 36695
LENGTH: 19
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SERBRAL INFORMATION:
APPLICANT: Dorn, Enin
APPLICANT: Rasmussen, Eric
TITLE OF INVENTION: DARMATMACOGENETIC DME Detection Assay Methods and Kits
FILE REFERENCE: FORS-07810
CURRENT APPLICATION NUMBER: US/10/354,953
CURRENT APPLICATION NUMBER: 1203-01-30
NUMBER OF SEQ ID NOS: 1120
SOFTWARE: Patentin version 3.2
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APPLICANT: LUKOWAAA, ALALEA
APPLICANT: Kurensky, David
TITILE OF INVENTION: Amplification Methods and Compositions
FILE REFERENCE: FORS-0696
CURRENT APPLICATION NUMBER: US/10/321,039
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: 09/998,157
PRIOR APPLICATION NUMBER: 60/329,113
PRIOR APPLICATION NUMBER: 60/329,113
PRIOR APPLICATION NUMBER: 60/320,489
PRIOR APPLICATION NUMBER: 60/360,489
PRIOR APPLICATION NUMBER: 60/360,489
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 759
SEQ ID NO 630
LENGTH: 18
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Best Local Similarity 88.2%; Pred. No. 5.1e+02;
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: Sequence 46, Application PC/TUS0013327
; GENERAL INFORMATION:
APPLICANT: McGrail, Maura
APPLICANT: Russell, Deanna L.
APPLICANT: Shartuck, Donna M.
APPLICANT: Shartuck, Donna M.
APPLICANT: Myziad Genetics, Inc.
TITLE OF INVENTION: DIABETES GENE
Sequence 630, Application US/10321039
GENERAL INFORMATION:
APPLICANT: Lyamichev, Victor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1296 GCCACAGAGCCTAGACA 1312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Synthetic US-10-354-953-757
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                                                                        Lukowiak, Andrew
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LENGTH: 18
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PCT-US03-05045-336

Sequence 336, Application PC/TUS0305045

GENERAL INFORMATION:
APPLICANT: Sirna Therapuetics Inc.
APPLICANT: Bejeglemni, Leconid
APPLICANT: Pavco, Pamela
APPLICANT: Pavco, Pamela
APPLICANT: Pavco, Pamela
APPLICANT: Posnaugh, Kathy
TITLE OF INVENTION: Receptor Gene Expression Using Short Interfering RNA
TITLE OF INVENTION: Receptor Gene Expression Using Short Interfering RNA
TITLE OF INVENTION: Receptor Gene Expression Using Short Interfering RNA
TITLE OF INVENTION NUMBER: US 60/393,924
PRIOR APPLICATION NUMBER: US 10/251,117
PRIOR FILING DATE: 2002-09-19
PRIOR FILING DATE: 2002-09-19
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
PCT-US03-05045-90
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ORGANISM: Artificial Sequence
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                                          Beigelman, Leonid
            McSwiggen, James
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Best Local Similarity 88.2
Matches 15; Conservative
                                      APPLICANT:
APPLICANT:
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                                      Strand = positive ConnectronObjectNumber = 39327
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APPLICANT: Formuly, Kathy
APPLICANT: Tomison, Sharon
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor
TITLE OF INVENTION: Receptor Gene Expression Using Short Interfering RNA
FILE REFERENCE: 400/081 (MBHB 02-468-B)
CURRENT APPLICATION NUMBER: PCT/US03/05045
CURRENT FILLING DATE: 2003-05-07
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THER INFORMATION: Description of Artificial Sequence: Target Sequence/sinA sense
PCT--US03-05-045-87
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PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-00-03
PRIOR FILING DATE: 2002-00-09
PRIOR FILING DATE: 2002-09-19
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-10-21
PRIOR FILING DATE: 2002-10-21
PRIOR PLING DATE: 2002-10-21
PRIOR PLING DATE: 2001-07-25
PRIOR PLING DATE: 2001-07-25
PRIOR PLING DATE: 2001-07-25
PRIOR PLING DATE: 2002-05-29
PRIOR FILING DATE: 2002-05-29
PRIOR PLING DATE: 2002-05-10
PRIOR PLING DATE: 2002-05-11
PRIOR PLING DATE: 2002-06-16
PRIOR PLING DAT
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0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                           0.6%; Score 13.8; DB 1; Length 19; 88.2%; Pred. No. 5.3e+02; rative 0; Mismatches 2; Indels
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PCT-US03-05045-90/c
Sequence 90, Application PC/TUS0305045;GENERAL INFORMATION:
APPLICANT: Sirna Therapuetics Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                 CT-US03-05045-87/c
Sequence 87, Application PC/TUS0305045
GENERAL INFORMATION:
APPLICANT: Sirna Therapuetics Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
APPLICANT: Pavco, Pamela
LOCATION: (3597227) ... (3597245)
, OTHER INFORMATION: Chromosome = 1
PCT-US02-25943-36695
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                                                                                                                           Query Match
Best Local Similarity
Matches 15; Conserv
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APPLICANT: Parco, Fathy
APPLICANT: Parco, Handle
APPLICANT: Posnaugh, Kathy
APPLICANT: Jamison, Sharon
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Facto:
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Facto:
TITLE OF INVENTION: RNA INTERFERS 1003-06-05
CURRENT FILING DATE: 2003-06-05
PRIOR PELLING DATE: 2002-07-03
PRIOR PELLING DATE: 2002-06-06
PRIOR PELLING DATE: 2002
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                                                        ; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region PCT-US03-05045-339
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0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                       Length 19;
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                                                                                                                                                                                                   Score 13.8; DB 1;
Pred. No. 5.3e+02;
2; Mismatches 2;
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PCT-US03-05045-524/c
; Sequence 5.24, Application PC/TUS0305045
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapuetics Inc.
; APPLICANT: Beigelman, James
; APPLICANT: Beigelman, Loonid
; APPLICANT: Paricelman, Loonid
; APPLICANT: Paricelman, Loonid
; APPLICANT: Paricelman, Loonid
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; Sequence 831, Application PC/TUS0305045
; GENERAL INFORMATION:
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                                                                                                                                                                                                            Query Match
Best Local Similarity 76.5%;
Matches 13; Conservative
ORGANISM: Artificial Sequence FEATURE:
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Pavco, Pamela
APPLICANT: Pavco, Pamela
APPLICANT: Pavco, Pamela
APPLICANT: Posnaudh, Kathy
TITLE OF INVENTION: Rathy
TITLE OF INVENTION: Receptor Gene Expression Using Short Interfering RNA
TITLE OF INVENTION: Receptor Gene Expression Using Short Interfering RNA
TITLE OF INVENTION: Receptor Gene Expression Using Short Interfering RNA
TITLE OF INVENTION: RUBBER: PCT/US03/05045
CURRENT APPLICATION NUMBER: US 60/393,924
PRIOR PELING DATE: 2002-07-03
PRIOR PELING DATE: 2002-07-03
PRIOR PELING DATE: 2002-06-19
PRIOR PILING DATE: 2002-06-19
PRIOR PELING DATE: 2002-06-19
PRIOR PELING DATE: 2002-06-19
PRIOR PELING DATE: 2002-06-19
PRIOR PELING DATE: 2002-06-10-21
PRIOR APPLICATION NUMBER: US 60/356,580
PRIOR PELING DATE: 2002-06-10-25
PRIOR PELING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 60/356,580
PRIOR PELING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: US 60/356,780
PRIOR PELING DATE: 2002-06-11
PRIOR PELING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: US 60/366,784
PRIOR PELING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: US 60/366,784
PRIOR PELING DATE: 2002-06-11
PRIOR PELING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/366,784
PRIOR PELING DATE: 2002-06-11
PRIOR PELING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/366,784
PRIOR PELING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/366,784
PRIOR PELING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/366,784
PRIOR PELING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/366,784
PRIOR PELING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/366,784
PRIOR PELING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/366,784
PRIOR PELING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/366,784
PRIOR PELING DATE: 2002-06-06
PRIOR PELING 
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             PRIOR APPLICATION NUMBER: US 09/916,466
PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2002-05-29
PRIOR FILING DATE: 2002-05-29
PRIOR FILING DATE: 2002-05-29
PRIOR PELICATION NUMBER: US 60/358,580
PRIOR PELICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR FILING DATE: 2002-03-11
PRIOR FILING DATE: 2002-03-11
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-29
PRIOR FILING DATE: 2002-06-29
PRIOR PRIOR SPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR PRIOR PRIOR APPLICATION 3.2
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NUMBER OF SEQ ID NOS: 1263
SOFTWARE: Patentin version 3.2
SEQ ID NO 339
LENGTH: 19
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0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 5.3e+02;
Matches 11; Conservative 4; Mismatches 2; Indels
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GENERAL INFORMATION:
APPLICANT: Sirna Therapuetics Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
APPLICANT: Pavco, Pamela
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US-10-016-490C-24/C
Sequence 24, Application US/10016490C
Sequence 24, Application US/10016490C
GENERAL INFORMATION:
APPLICANT: Yin, James Q.
TITLE OF INVENTION: Methods for design and selection of short double-stranded
TITLE OF INVENTION: 0.1igonucleotides, and compounds of gene drugs
FILE REFERENCE: 01-2793
CURRENT FILIAGO BATE: 2002-11-22
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.1
                                                                                                                    Gaps
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Pred. No. 5.3e+02;
0; Mismatches 2; Indels
                                                                   Length 19;
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                                                                                                               2; Indels
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                                                           0.6%; Score 13.8; DB 1;
88.2%; Pred. No. 5.3e+02;
Live 0; Mismatches 2;
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88.2%; Pred. No. 5.3e+02;
live 0; Mismatches 2;
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US-10-016-490C-24
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: McGrail, Maura
APPLICANT: Russell, Deanna L.
APPLICANT: Russell, Deanna L.
APPLICANT: Shatuck, Donna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: DIABETES GENE
FILE REFERENCE: Diabetes Gene III
CURRENT PPLICATION NUMBER: US/09/573,425
CURRENT FILING DATE: 2000-01-06
PRIOR APPLICATION NUMBER: US 60/174,700
PRIOR FILING DATE: 2000-01-06
PRIOR FILING DATE: 1999-05-21
NUMBER: OF SEQ ID NOS: 68
SEQ ID NO 48
                                                                                                                                                                                                                                                                                                                                 Sequence 48, Application US/09573425
GENERAL INFORMATION:
APPLICANT: McGrail, Maura
                                                                                                                                                           1263 CCCCCTTCAGAAGTGGG 1279
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.2
Matches 15; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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US-09-573-425-48
                                                           Query Match
Best Local Similarity
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US-09-573-425-48/c
          US-09-573-425-46
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LENGTH: 19
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                                                                                             APPLICANT: Fosnaugh, Kathy
APPLICANT: Jamison, Sharon
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor
TITLE OF INVENTION: Receptor Gene Expression Using Short Interfering RNA
FILE REFERENCE: 400/081 (MBHB 02-468-B)
CURRENT APPLICATION NUMBER: PCT/US03/05045
CURRENT FILING DATE: 2003-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region PCT-US03-05045-831
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SOSTWARE: Patentin version 3.2
SEQ ID NO 831
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llarity 64.7%; Pred. No. 5.3e+02;
Conservative 4; Mismatches 2; Indels
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APPLICANT: McGrail, Maura
APPLICANT: Russell, Deanna L.
APPLICANT: Shattuck, Donna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: DIABETES GENE
FILLE REFERENCE: Diabetes Gene III
CURRENT APPLICATION NUMBER: US/09/573,425
CURRENT FILING DATE: 2000-05-16
                                                                                                                                                                                                                                    CURRENT FILING DATE: 2003-05-07
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR PILING DATE: 2002-07-03
PRIOR PILING DATE: 2002-09-19
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 10/163,522
PRIOR PILING DATE: 2001-07-25
PRIOR PILING DATE: 2001-07-25
PRIOR PILING DATE: 2001-07-25
PRIOR PRILING DATE: 2002-06-29
PRIOR PILING DATE: 2002-06-29
PRIOR PILING DATE: 2002-06-29
PRIOR PILING DATE: 2002-06-30
PRIOR PILING DATE: 2002-06-30
PRIOR PILING DATE: 2002-06-30
PRIOR PILING DATE: 2002-06-31
PRIOR PILING DATE: 2002-06-32
PRIOR PILING DATE: 2002-06-32
PRIOR PILING DATE: 2002-06-32
PRIOR PILING DATE: 2002-06-32
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PRIOR APPLICATION NUMBER: 2.00

PRIOR FILING DATE: 1999-05-21

NUMBER OF SEQ ID NOS: 68

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 46

LENGTH: 19
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Sirna Therapuetics Inc
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                                                                        Pavco, Pamela
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ORGANISM: Homo sapiens
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Hest Local Similarity
Thes 11; Conserva
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US-09-573-425-46/c
                                                                      APPLICANT:
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APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor
TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
FILE REFERENCE: 900/042 (MBHB02-468-A)
CURRENT APPLICATION NUMBER: US/10/251,117
CURRENT FILING DATE: 2003-02-24
PRIOR PELING DATE: 2002-07-03
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-07-05
PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 1213
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RAR Interference Mediated Inhibition of Epidermal Growth Facto:
TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
FILE REFERENCE: 900/042 (MEHBO2-468-A)
FILE REFERENCE: 900/042 (MEHBO2-468-A)
CURRENT APPLICATION NUMBER: US 10/1/251,117
CURRENT FILING DATE: 2002-02-4
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR APPLICATION NUMBER: US 60/398,580
PRIOR PELING DATE: 2002-06-06
PRIOR PELING DATE: 2002-02-06
PRIOR PELING DATE: 2001-02-25
PRIOR PELING DATE: 2001-07-25
PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 1213
SOFTWARE: Patentin Version 3.0
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0.6%; Score 13.8; DB 1;
Best Local Similarity 64.7%; Pred. No. 5.3e+02;
Matches 11; Conservative 4; Mismatches 2;
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 336, Application US/10251117; GENERAL INFORMATION:
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LENGTH: 19
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; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 39327
US-10-227-565-36695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MCSWiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor
TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
FILE REFERENCE: 90/042 (MBHB02-468-A)
CURRENT APPLICATION NUMBER: US/10/251,117
CURRENT FILING DATE: 2003-02-24
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                                                                                          APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REPERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/227,565
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SOFTWARE: Proprietary
SEQ ID NO 36695
LENGTH: 19
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88.2%; Pred. No. 5.3e+02;
tive 0; Mismatches 2; Indels
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88.2%; Pred. No. 5.3e+02;
cive 0; Mismatches 2; Indels
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PRIOR APPLICATION NUMBER: US 60/393,924

PRIOR APPLICATION NUMBER: US 60/393,924

PRIOR FILING DATE: 2002-06-06

PRIOR FILING DATE: 2002-06-06

PRIOR FILING DATE: 2002-06-06

PRIOR FILING DATE: 2002-02-07

PRIOR FILING DATE: 2001-07-25

PRIOR FILING DATE: 2001-07-25

PRIOR FILING DATE: 2001-07-25

PRIOR FILING DATE: 2001-07-25

PRIOR FILING DATE: 2001-06-06

NUMBER OF SEQ ID NOS: 1213

SOFURARE: PATENTIN VERSION 3.0

LENGTH: 19
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                                              Sequence 36695, Application US/10227565 GENERAL INFORMATION:
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Sequence 90, Application US/10251117
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.2%
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Best Local Similarity 88.29
Matches 15, Conservative
            -10-227-565-36695
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OTHER INFORMATION: Description of Artificial Sequence: sinh antisense region
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               Length 19;
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0.6%; Score 13.8; DB 1; Length 1
Best Local Similarity 64.7%; Pred. No. 5.3e+02;
Matches 11; Conservative 4; Mismatches 2; Indels
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GENERAL INFORMATION:

APPLICANT: GOFF, STEPHEN

APPLICANT: BONAN, CAROLINE

APPLICANT: BONAN, CAROLINE

APPLICANT: WANG, RONG-LIN

TITLE OF INVENTION: ERREAT MARKERS AND THEIR USES

TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES

TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES

FILE REFERENCE: NADII.058C1

CURRENT APPLICATION NUMBER: US 10/266,090

PRIOR APPLICATION NUMBER: US 00/326,117

PRIOR APPLICATION NUMBER: US 60/326,117

PRIOR RILING DATE: 2001-09-26

NUMBER OF SEQ ID NOS: 51812

SOFTHARE: FASTERQ for Windows Version 4.0
Query Match

0.6%; Score 13.8; DB 1;
Best Local Similarity 88.2%; Pred. No. 5.38+02;
Matches 15; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 885, Application US/10251117
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
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ORGANISM: Artificial Sequence
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                                                                                                                                                858 TGTTAAGGGCACTGAGG
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LENGTH: 19
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                                                                                                                                                                                   APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwiggen, James

TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor F

TITLE OF INVENTION: Gene Expression Using Short Interfering RNA

TITLE OF INVENTION: Gene Expression Using Short Interfering RNA

CURRENT APPLICATION NUMBER: US/10/251,117

CURRENT APPLICATION NUMBER: US 60/393,924

PRIOR FILING DATE: 2002-06-06

PRIOR FILING DATE: 2002-06-06

PRIOR FILING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: US 60/358,580

PRIOR FILING DATE: 2001-07-25

PRIOR FILING DATE: 2001-07-26

PRIOR FILING DATE: 2001-07-36

PRIOR APPLICATION NUMBER: US 60/296,249

PRIOR PLING DATE: 2001-07-36

PRIOR APPLICATION NUMBER: US 60/296,249

PRIOR APPLICATION NUMBER: US 60/296,249
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GENERAL STATE STATE THATE APPLICANT:
GENERAL STATE STATE STATE STATE STATE STATE STATE OF INVENTION:
FILE OF INVENTION:
GURRENT APPLICATION NUMBER: US/10/251,117
CURRENT APPLICATION NUMBER: US 60/393,924
FRIOR FILING DATE: 2002-07-03
FRIOR FILING DATE: 2002-06-06
FRIOR FILING DATE: 2002-02-20
FRIOR FILING DATE: 2002-02-20
FRIOR FILING DATE: 2001-07-25
FRIOR FILING DATE: 2001-
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                                                                                     S-10-251-117-339
Sequence 339, Application US/10251117
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 13; Conservative
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LENGTH: 19
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US-10-310-188-10574/c
| Sequence 10574, Application US/10310188
| Sequence 10574, Application US/10310188
| GENERAL INPORMATION:
| APPLICANT: RosettaGenonics
| TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G:
| TITLE OF INVENTION: USES THEREOF
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GENERAL INFORMATION:
APPLICANT: ROSELEGGEMODICS
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION UTHBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE PATENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                          Score 13.8; DB 1; Length 19; Pred. No. 5.3e+02;
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Best Local Similarity 88.2%; Pred. No. 5.3e+02;
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88.2%; Pred. No. 5.3e+02;
Live 0; Mismatches 2;
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                                     FILE REFERENCE: 47487
CURRENT PEPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1678
LENGTH: 19
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         TITLE OF INVENTION: USES THEREOF
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ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-10-310-188-10574
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 15; Conservat
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Best Local Similarity
Matches 15; Conserva
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US-10-310-188-6272
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LENGTH: 19
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; APPLICANT: RosettaGemonics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6274, Application US/10293338
GENERAL INFORMATION:
TITLE OF INVENTION: BIOINFORMATICALLY
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE REFERENCE: 45282
CURRENT APPLICATION NUMBER: US/10/293,338
CURRENT FILLENG DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 8785
SOFTWARE: Patentin version 3.1
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
FILE REPERBNCE: 47416
CURRENT APPLICATION NUMBER: US/10/303,778
CURRENT FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 17608
SOFTWARE: Patentin version 3.1
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                        ; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA US-10-266-090-46529
                                                                                                                            Length 19;
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                                                                                                             Query Match 0.6%; Score 13.8; DB 1; Length 1 Best Local Similarity 88.2%; Pred. No. 5.3e+02; Matches 15; Conservative 0; Mismatches 2; Indels
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88.2%; Pred. No. 5.3e+02;
rative 0; Mismatches 2; Indels
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88.2%; Pred. No. 5.3e+02;
trive 0; Mismatches 2;
                                                                                                                                                                                                                                       1134 CACCTCCAGCTCCACCT 1150
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                                                                                                                                                                                                                                                                            TCTTTTTTTTTCCC
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Best Local Similarity 88.2°
Matches 15; Conservative
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US-10-293-338-6274
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 15; Conserv
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LENGTH: 19
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FEATURE:
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Sequence 72814, Application US/10310188
GENERAL INFORMATION:
APPLICANT: ROSECTAGEMONICS
TITLE OF INVENTION: USES THEREOF
CURRENT APPLICATION NUMBER: US/10/310,188
                                                                                                                                                                                                                                                               APPLICANT: RosettaGemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT APPLICATION NUMBER: US/10/310,188
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 86841
SEQ ID NO 34905
LENGTH: 19
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| Sequence 72813, Application US/10310188
| GENERAL INFORMATION:
| APPLICANT: RosettaGemonics
| TITLE OF INVENTION: USES THEREOF
| CURRENT PAPLICATION NUMBER: US/10/310,188
| CURRENT PILING DATE: 2002-12-19
| NUMBER OF SEQ ID NOS: 86841
| SOFTWARE: PatentIn version 3.1
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                                           2; Indels
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18.2%; Pred. No. 5.3e+02;
ve 0; Mismatches 2;
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Pred. No. 5.3e+02;
0; Mismatches 2;
    Score 13.8; DB 1;
Pred. No. 5.3e+02;
                                           0; Mismatches
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US-10-310-188-34905/c
; Sequence 34905, Application US/10310188
; GENERAL INFORMATION:
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Best Local Similarity 86.2.
Thes 15; Conservative
Query Match 0.67
Best Local Similarity 88.23
Matches 15; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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US~10-310-188-34905
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US-10-310-188-72814/c
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LENGTH: 19
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
TITLE REFERENCE: 47487
CURRENT FAPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SSQ ID NO 23028
LENGTH: 19
                                                                                            APPLICANT: Rosettagemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 19123
LENGTH: 19
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Pred. No. 5.3e+02;
0; Mismatches 2;
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                                                          Sequence 18123, Application US/10310188 GENERAL INFORMATION:
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Matches 15; Conservative
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; ORGANISM: Homo sapiens
US-10-310-188-33554
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ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-10-310-188-23028
                                      US-10-310-188-18123/c
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APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
APPLICANT: Dufeare-Gare, Isabelle
APPLICANT: Dufeare-Gare, Isabelle
TITLE OF INVENTION: BIALIELIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY.
FILE REFERENCE: 84.US1.PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (3597227)...(3597245)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 392
US-10-367-832A-36695
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                                                                     APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PAO1, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/367,832A
CURRENT PILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SOFTWARE: Proprietary
SEQ ID NO 36695
LENĞTH: 19
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TITLE OF INVENTION: Method, Composition and Kit for Typing
TITLE OF INVENTION: Classical HiA Class I Genes
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Oppedahl & Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 19;
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Pred. No. 5.3e+02;
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Best Local Similarity 88.2%; Pred. No. 5.3e+02;
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1992 Commerce Street Suite 309
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CURRENT FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 13665
SOFTWARE: Patent.pm
                          Sequence 36695, Application US/10367832A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 8300, Application US/60216745; GENERAL INFORMATION: APPLICANT: Cohen, Daniel APPLICANT: Blumenfeld, Marta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 2, Application US/08729043; GENERAL INFORMATION:
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Best Local Similarity 88.2%;
Matches 15; Conservative (
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US-60-216-745-8300/c
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US-08-729-043-2
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
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Sequence 75577, Application US/10310188

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

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TITLE OF INVENTION:

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TITLE OF INVENTION:

USES THEREOF

TITLE OF INVENTION:

TOTRENT PPLICATION NUMBER: US/10/310,188

CURRENT FILING DATE: 2002-12-19

NUMBER OF SEQ ID NOS: 86641

SOFTWARE: PATENTIN VENTION 3.1

SEQ ID NO 75577
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88.2%; Pred. No. 5.3e+02;
iive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                       0.6%; Score 13.8; DB 1; Length 19; 88.2%; Pred. No. 5.3e+02;
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   2002-12-19
86841
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CURRENT FILING DATE: 2002-12-1
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 72814
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Matches 15; Conservative
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Matches 15; Conserv
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Matches 15; Conserv
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US-10-310-188-78419/c
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Strand = positive ConnectronObjectNumber = 118
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                                                                                                                                                 PCT-USO2-25944-7448

Sequence 7448, Application PC/TUSO225944

GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
FILE REPREBNCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PCT/USO2/25944

CURRENT FILING DATE: 2002-08-27

NUMBER OF SEQ ID NOS: 9208

SOFURMARE: Proprietary
SEQ ID NO 7448

LENGTH: 15
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GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants,
TITLE OF INVENTION: Saccharomyces cerevisiae complete (FILE REPRENCE: Jim Zegeer Law Offices - 703-684-8333; CURRENT APPLICATION NUMBER: US/10/227,564
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 9208
SOFTWARE: Proprietary
SEQ ID NO 7396
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Saccharomyces cerevisiae complete genome.
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ORGANISM: Saccharomyces cerevisiae complete genome
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93.3%; Pred. No. 4.8e+02;
tive 0; Mismatches 1;
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OTHER INFORMATION: Chromosome =13

PCT-US02-25944-7448
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, CTHER INFORMATION: Chromosome =11
US-10-227-564-7396
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Best Local Similarity
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Best Local Similarity
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US-10-227-564-7396
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TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CORRENT APPLICATION NUMBER: PCT/US02/25944
CURRENT FILIG DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 9208
SOFTWARE: Proprietary
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                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
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ORGANISM: Saccharomyces cerevisiae complete genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: VGEN.P-037-US
TELECOMMUTICATION: IMPORMATION:
TELEPHONE: (914) 245-3252
TELEPRAX: (914) 962-4330
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                                                                                                                                                                           SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,043
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: other nucleic acid
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                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                              IBM compatible
SYSTEM: MS DOS
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STRANDEDNESS: double
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) OTHER INFORMATION:
US-08-729-043-2
                                                                                                                              COMPUTER: IBM COM
OPERATING SYSTEM:
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Best Local Similarity
Matches 14; Conserv
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ORGANISM: human
Yorktown
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LENGTH: 15
                                          COUNTRY:
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PCT-US03-40978-73653/c

Sequence 73653, Application PC/TUS0340978

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLO01499

CURRENT APPLICATION NUMBER: PCT/US03/40978

CURRENT PILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73397

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 73653
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i OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = PCT-US02-25940-3485
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TILE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmi
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TILE REPERBNCE.
TOTALICATION NUMBER: PCT/US02/25940
CURRENT APPLICATION NUMBER: PCT/US02/25940
CURRENT FILING DATE: 2002-08-27
SOFTWARE: Proprietary
SEQ ID NO 3485
LENGTH: 16
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0.6%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 1;
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93.3%; Pred. No. 5.2e+02;
tive 0; Mismatches 1;
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; Sequence 10, Application US/09573684
; GENERAL INFORMATION:
; APPLICANT: HOVANEZ, TIMOTHY A.
; APPLICANT: BURKELL, PAUL C.
; TITLE OF INVENTION: AMMONIA-OXIDIZING BACTERIA; FILE REFERENCE: 81289/264667/ASH
; CURRENT APPLICATION NUMBER: US/09/573,684
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.1
                                                                                                                                           PCT-US02-25940-3485; Sequence 3485, Application PC/TUS0225940; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Deinococcus radiodurans R1
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1097 CCACCCTGGGCTTCA 1111
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; ORGANISM: Homo sapiens
PCT-US03-40978-73653
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Best Local Similarity
Matches 14; Conserv
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CHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 11378
US-10-287-787-10375
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US-10-287-787-11243
                                                                                                                                                                                            Strand = positive ConnectronObjectNumber = 11860
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TITLE OF INVENTION: Caulobacter crescentus complete genome.
FILE REFERENCE: Jim Zeqeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/287,787
CURRENT FILMS DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 27958
SOFTWARE: Proprietary
SEQ ID NO 10375
LENGTH: 15
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TITLE OF INVENTION: Caulobacter crescentus complete genome.
FILE REPERBUCE: Jun Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/287,787
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 27958
SOFTWARE: Proprietary
LENGTH: 15
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                                                                                                                      complete genome
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; Sequence 10375, Application US/10287787
; GENERAL INFORMATION:
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                                                                                          TYPE: DNA ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                             | LOCATION: (641065)...(641079)
| OTHER INFORMATION: Chromosome =13
| US-10-227-564-7448
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Best Local Similarity 93.33
Matches 14; Conservative
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NUMBER OF SEQ ID NOS: 9208
                    SOFTWARE: Proprietary
SEQ ID NO 7448
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Best Local Similarity
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Sequence 78695, Application US/10310188
GENERAL INFORMATION:
APPLICANT: ROSettaGemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GRILLE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
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GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmi
FILM REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/367,892
CURRENT FILMS DATE: 2003-03-06
NUMBER OF SEQ ID NOS: 25502
SOFTWARR: Proprietary
SEQ ID NO 3485
LENGTH: 16
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US-10-659-948A-10/C

Sequence 10, Application US/10659948A

Sequence IN, Application US/10659948A

MEDICANT: HOVANEC, Timothy A

TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria

FILE REFERENCE: 81289-294309

CURRENT APPLICATION NUMBER: US/10/659,948A

PRIOR APPLICATION NUMBER: US/10/659,948A

PRIOR APLICATION NUMBER: US 09/573,684

PRIOR PLING DATE: 2000-05-19

PRIOR PLING DATE: 2002-09-19

PRIOR PLING DATE: 2002-09-19

PRIOR FILING DATE: 2002-09-19
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Pred. No. 5.2e+02;
0; Mismatches 1;
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93.3%; Pred
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OTHER INFORMATION: Chromosome = 1
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Best Local Similarity 93.3°
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                               US-10-310-188-78695/c
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US-10-367-892-3485
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LENGTH: 16
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COTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = US-10-227-563-3485
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OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber
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TITLE OF INVENTION: Helicobacter pylori 26695 complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION WIBER: US/10/294,040
CURRENT FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1102
                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-573-684-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmi
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                                                                                                                                                                                              Length 16
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FILE OF INVENTION: Delinococus radiodurans R1 completer FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333 CURRENT PRILING DATE: 2002-08-26

NUMBER OF SEQ ID NOS: 25502

SOFTWARE: Proprietary

SEQ ID NO 3485

LENGTH: 16
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0.6%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 1;
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0.6%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                   1184 CCCGCAGAGAGGTGG 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1235 CAGCCCTCGCCTCCG 1249
                                               TYPE: DNA ORGANISM: Artificial Sequence
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SEQ ID NO 85
LENGTH: 16
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Best Local Similarity
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SEQ ID NO 10
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                                                                                              FEATURE:
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: Mcxiggen, Jim
APPLICANTON TWHER: US/09/531,025A
TITLE REFERENCE: MHH800-845-E (24/7277)
CURRENT APPLICATION NUMBER: US 08/433,933
FRIOR APPLICATION NUMBER: US 08/434,504
FRIOR FILING DATE: 1995-05-04
FRIOR APPLICATION NUMBER: US 08/434,504
FRIOR APPLICATION NUMBER: US 08/436,430
                                                                                                                                                                                                                                                                                                                                                                     PCT-US03-40978-73370/C

FCT-US03-40978-73370, Application PC/TUS0340978

SEQUENCE 73370, Application PC/TUS0340978

GENERAL INFORMATION:
TITLE OF INVENTION: GENERAL INFARCTION, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLO01499

CURRENT APPLICATION NUMBER: PCT/US03/40978

CURRENT APPLICATION NUMBER: PCT/US03/40978

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: FastEQ for Windows Version 4.0

SOFTWARE: FastEQ for Windows Version 4.0
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                                                                           Score 13.4; DB 1;
Pred. No. 5.2e+02;
0; Mismatches 1;
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93.3%; Pred. No. 5.5e+02;
iive 0; Mismatches 1;
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                                                  0.6%; Scor.
93.3%; Pred
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ORGANISM: Hepatitis B virus
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Best Local Similarity 93.33
Matches 14; Conservative
                                                                        Query Match
Best Local Similarity 93.33
Matches 14; Conservative
                                                                                                                                                                                                                                                                                      16 rrcrccrccAGcrcc
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US03-40978-73370
          US-10-741-600-73653
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 73653
LENGTH: 16
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INCOLUMNITATION:
TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria
FILE REPRENCES: 81289-284781
CURRENT APPLICATION NUMBER: US/10/659,980A
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: US 09/573,684
PRIOR APPLICATION NUMBER: US 09/573,684
PRIOR APPLICATION NUMBER: US 60/386,217
PRIOR APPLICATION NUMBER: US 60/386,219
PRIOR FILING DATE: 2002-09-19
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0.6%; Score 13.4; DB 1; Length 16;

Best Local Similarity 93.3%; Pred. No. 5.2e+02;

Matches 14; Conservative 0; Mismatches 1; Indels
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PRIOR APPLICATION NUMBER: US 60/386,219
PRIOR FILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.2
SEQ ID NO 10
LENGTH: 16
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US-10-659-980A-10/c
; Sequence 10, Application US/10659980A
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: PCR primer US-10-659-948A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                 ORGANISM: Artificial
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APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules
FILE REPERENCE: 237/193
CURRENT APPLICATION NUMBER: US/09/546,745A
CURRENT FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 7043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lipshitz, Robert J.
APPLICANT: Lipshitz, Robert J.
APPLICANT: Daley, George Q.
TITLE OF INVENTION: CHARACTERIZATION OF SINGLE NUCLEOTIDE
TITLE OF INVENTION: POLYMORPHISMS IN CODING REGIONS OF HUMAN GENES
FILE REPERENCE: 2825.1011-003
CURRENT APPLICATION NUMBER: US/09/541,946
CURRENT FILING DATE: 1990-03-31
PRIOR APPLICATION NUMBER: US 60/127,248
PRIOR FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 2889
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 1659
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                           0.6%; Score 13.4; DB 1;
93.3%; Pred. No. 5.5e+02;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.6%; Score 13.4; DB 1; Best Local Similarity 93.3%; Pred. No. 5.5e+02; Matches 14; Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: Oligonucleotide primer US-09-541-946-1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ribozyme Pharmaceuticals, Inc. APPLICANT: Blatt, Larry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-546-745A-6637; Sequence 6637, Application US/09546745A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            RESULT 866
US-09-541-946-1659/c
; Sequence 1659, Application US/09541946
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lander, Eric S.
APPLICANT: Cardill, Michele
APPLICANT: Altshuler, David M.
APPLICANT: Ireland, James S.
APPLICANT: Sklar, Pamela
APPLICANT: Patil, Nila
                                                                                                                                                               1073 TCAGTCCCACTCCAG 1087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                               15 TGAGTCCCACTCCAG 1
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                              Query Match
Best Local Similarity 93.33
Matches 14; Conservative
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Best Local Similarity
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LENGTH: 17
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APPLICANT: Blatt, Larry
APPLICANT: McEvigen, June
APPLICANT: McEvigen, June
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REPRENCE: MBHENDO-845-E (247/277)
CURRENT APPLICATION NUMBER: US 0/9/531,025A
CURRENT APPLICATION NUMBER: US 08/193,627
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 08/434,504
PRIOR FILING DATE: 1995-05-04
PRIOR FILING DATE: 1995-05-04
PRIOR FILING DATE: 1999-11-08
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6341
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1602
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SEMERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Lander, Lan
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26.7%; Pred. No. 5.5e+02;
tive 10; Mismatches 1; Indels
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, OTHER INFORMATION: Oligonucleotide primer US-09-541-946-1657
                                                                                                                                                                                                                  Sequence 1602, Application US/09531025A GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
907 ATTITCTTIGGICTT 921
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ORGANISM: Hepatitis B virus
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Matches 4; Conserv
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US-09-541-946-1657/c
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APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
FILE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE OF INVENTION NUMBER: US 09/636,385
CURRENT APPLICANTON NUMBER: US 09/531,025
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1994-11-08
NUMBER OF SEQ ID NOS: 6341
SCHWARRE: Patentin version 3.0
IENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Draper, Ken
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inibiting Hepatitis B Virus Replication
FILE REPERENCE: 400,001
CURRENT APPLICATION NUMBER: US/09/696,347
CURRENT FILING DATE: 2000-10-24
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0.6%; Score 13.4; DB 1;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1;
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PRIOR APPLICATION NUMBER: US 09/636,385

PRIOR FILING DATE: 2000-08-09

PRIOR FILING DATE: 2000-08-09

PRIOR FILING DATE: 2000-03-20

PRIOR FILING DATE: 2000-03-20

PRIOR APPLICATION NUMBER: US 09/831,025

PRIOR FILING DATE: 1994-02-07

PRIOR FILING DATE: 1994-02-07

PRIOR FILING DATE: 1995-05-04

PRIOR FILING DATE: 1995-05-04

PRIOR PILING DATE: 1995-05-04

PRIOR FILING DATE: 1999-11-08

NUMBER OF SEQ ID NOS: 6389

SEQ ID NO 909

LENGTH: 17
                                                                                                                                                                                      APPLICANT: Ribozyme Pharmaceuticals, Inc
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                                                                                                                         ; Sequence 1602, Application US/09636385; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 909, Application US/09696347; GENERAL INFORMATION:
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     3 AUTUUCUTUUGUCUU 17
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                                                                             RESULT 870
US-09-636-385-1602
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APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REPERSENCE: MBHB00-845-F (250/125)
CURRENT APPLICANTON NUMBER: US/09/636,385
CURRENT FILING DATE: 1992-05-14
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6341
SOSTWARE: PatentIn version 3.0
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     Gaps
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McLaughen, Jim
APPLICANT: WcLaughen, Jim
APPLICANT: Won Carlowitz, Ira
APPLICANT: WcLaughlin, Fiona
APPLICANT: Randi, Anna Maria
TITLE OF INVENTION: Method and Reagent for the Inhibition of ERG
FILE REFERENCE: 229,006
FILE REFERENCE: 229,006
CURRENT FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 5366
SOFTWARE: Patentin version 3.0
SEQ ID NO 1505
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Mismatches
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
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                                                 1065 CCCAAGCTTCAGTCC 1079
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ORGANISM: Hepatitis B Virus
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Best Local Similarity 93.33
Matches 14; Conservative
Conservative
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                                                                                                                                                                                RESULT 868
US-09-572-021-1505/c
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US-09-636-385-909
11;
Matches
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Sequence 559, Application US/09818875

Sequence 559, Application US/09818875

Sequence 559, Application US/09818875

Sequence 559, Application US/09818875

APPLICANT: Kmiec, Eric B.

APPLICANT: Race, Michael C.

TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single TITLE OF INVENTION: Stranded Oligonucleotides

FILE REPERBECE: Napro-4

CURRENT APPLICATION NUMBER: US/09/818,875

CURRENT APPLICATION NUMBER: US 60/192,176

PRIOR FILING DATE: 2000-03-27

PRIOR APPLICATION NUMBER: US 60/192,179

PRIOR APPLICATION NUMBER: US 60/208,538

PRIOR APPLICATION NUMBER: US 60/244,989

PRIOR APPLICATION NUMBER: US 60/244,989

NUMBER OF SEQ ID NOS: 4385

SOFTWARE: Friedman macro Napro4

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GENERAL INFORMATION:
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Browning. Bharat
APPLICANT: Hackerli, Pere
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REPERBENCE NBHARA (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
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Pred. No. 5.5e+02;
0; Mismatches 1;
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PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SEQ ID NO 2377
LENGTH: 17
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Best Local Similarity 93.3%; Pr.
Matches 14; Conservative 0;
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US-09-780-533A-2377
                                                                                                               sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
; SEQ ID NO 1806
; LENGTH: 17
; TYPE: RNA
; ORGANISM: HOMO SA
US-09-780-533A-1806
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US-09-818-875-559/c
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APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inibiting Hepatitis B Virus Replication
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APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Convering Bharat
APPLICANT: Haeberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER: OF SEQ. DE NOS: 6679
                                                                                                                                                                        Gaps
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                                                                                                        Length 17;
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                                                                                                 Score 13.4; DB 1;
Pred. No. 5.5e+02;
                                                                                                                                                                 Mismatches
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CURRENT FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 09/636,347
CURRENT FILING DATE: 2000-10-24
PRIOR PLING DATE: 2000-09-09
PRIOR FILING DATE: 2000-03-20
PRIOR PLING DATE: 2000-03-20
PRIOR PLING DATE: 1900-03-20
PRIOR PLING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1995-05-04
PRIOR FILING DATE: 1995-05-04
PRIOR PLING DATE: 1995-05-04
PRIOR PLING DATE: 1995-05-04
PRIOR PLING DATE: 1995-05-04
PRIOR PLING DATE: 1995-05-04
PRIOR FILING DATE: 1995-05-05
PRIOR PRIOR DATE: 1995-05-05
PRIOR PRIOR DATE: 1995-05-05
PRIOR PRIOR PRIOR DATE: 199
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ribozyme Pharmaceuticals, Inc.
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                                                                0.6%; Sc._
26.7%; Pred
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   ORGANISM: Hepatitis B Virus
                                                                                                                                                                 4; Conservative
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                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
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          ; ORGANISM: нер.
US-09-696-347-909
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APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McNatggen, Jim
APPLICANT: McNatggen, Jim
APPLICANT: McNatggen, Jim
APPLICANT: McNatggen, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
CURRENT APPLICATION NUMBER: US/09/877,478
CURRENT FILING DATE: 2001-12-31
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                                                                                                                                                                                                                                                                                                                                Query Match 0.6%; Score 13.4; DB 1; Length 17; Best Local Similarity 26.7%; Pred. No. 5.5e+02; Matches 4; Conservative 10; Mismatches 1; Indels
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26.7%; Pred. No. 5.5e+02;
tive 10; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 1992-05-14
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 1090-07
PRIOR FILING DATE: 1995-05-04
PRIOR FILING DATE: 1995-11-08
NUMBER: PREDICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6586
SOFTWARE: PATCHTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1602, Application US/09877478; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
PRIOR APPLICATION NUMBER: US 08/434,504
PRIOR FILING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6586
SCFTWARE: Patentin version 3.0
SEQ ID NO 909
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APPLICANT: Gu, Yizhong
APPLICANT: Nguyen, Cung-Tuong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          909 TTTCTTTGGTCTTTG 923
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1 UUUCUUUUGUCUUUG 15
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                                                                                                                                                                                                                 TYPE: RNA
CRGANISM: Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis B virus
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Best Local Similarity
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US-09-877-478-1602
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, Jim
APPLICANT: McMager, Us/09/029
TITLE OF INVENTION: McHod and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: MBHB00-445-H (400/029)
CURRENT APPLICATION NUMBER: US 07/892,712
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR PILING DATE: 2000-03-20
PRIOR PILING DATE: 2000-03-20
PRIOR PILING DATE: 2000-03-20
PRIOR PILING DATE: 2000-010-24
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1995-05-04
PRIOR FILING DATE: 1995-05-04
                                                                                                                                                                                                                                                                                                                       Sequence 560, Application US/09818875

Sequence 560, Application US/09818875

Sequence 560, Application US/09818875

Sequence 560, Application US/09818875

APPLICANT: Raice, Brich B.

APPLICANT: Raice, Michael C.

TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single TITLE OF INVENTION: Stranded Oligonucleotides

FILE REFERENCE: Napro-4

CURRENT APPLICATION NUMBER: US/09/818,875

CURRENT PILING DATE: 2001-03-27

PRIOR FILING DATE: 2000-03-27

PRIOR FILING DATE: 2000-03-27

PRIOR PLING DATE: 2000-06-01

PRIOR FILING DATE: 2000-06-01

SEQ ID NOS: 4385

SEQ ID NOS: 4385

SEQ ID NOS: 4385

SEQ ID NO 560
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                                                     0.6%; Score 13.4; DB 1; Length 17; ilarity 93.3%; Pred. No. 5.5e+02; Conservative 0; Mismatches 1; Indels
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ORGANISM: Homo sapiens
                                                                                  Local Similarity
les 14; Conserv
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     US-09-818-875-559
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Sequence 559, Application US/10209787

GENERAL INFORMATION:
APPLICANT: Raiec, Eric B.
APPLICANT: Raiec, Eric B.
APPLICANT: Gamper, Howard B.
APPLICANT: Acie, Michael C.
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single TITLE OF INVENTION: Stranded Oligonucleotides
FILE REFERENCE: Nato-4
CURRENT APPLICATION NUMBER: US/10/209,787
CURRENT APPLICATION NUMBER: US 09/818,875
PRIOR APPLICATION NUMBER: US 60/192,176
PRIOR APPLICATION NUMBER: US 60/192,176
PRIOR APPLICATION NUMBER: US 60/192,176
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: US 60/208,538
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: US 60/244,989
NUMBER OF SEQ ID NOS: 4385
SOCTWARE: Friedman macro Napro4
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APPLICANT: Kamiec Eric B.
APPLICANT: Kamiec File B.
APPLICANT: Raper. Howard B.
APPLICANT: Raper C.
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
TITLE OF INVENTION: Stranded Oligonucleotides
FILE REFERENCE: Napro-730
FILE REPERINGE: Napro-730
CURRENT FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: US 09/818,875
PRIOR APPLICATION NUMBER: US 60/192,176
PRIOR APPLICATION NUMBER: US 60/192,179
PRIOR APPLICATION NUMBER: US 60/192,179
PRIOR PILING DATE: 2000-03-27
PRIOR PILING DATE: 2000-06-01
PRIOR FILING DATE: 2000-06-01
PRIOR FILING DATE: 2000-06-01
PRIOR FILING DATE: 2000-06-01
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          Mismatches
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SEQ ID NO 560
LENGTH: 17
TYPE: DNA
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US-10-209-787-559
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US-10-209-787-559/c
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Best Local S:
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93.3%; Pred. No. 5.5e+02;
tive 0; Mismatches 1; Indels
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gu, Yizhon:
TITLE OF INVENTION:
FILE REFERENCE: PRO169
CURRENT APPLICATION NUMBER: US/10/060,830
CURRENT APPLICATION NUMBER: US/10/060,830
CURRENT APPLICATION NUMBER: PCT/US01/00667
FRIOR PILING DATE: 2001-01-30
FRIOR FILING DATE: 2001-01-30
TITLE OF INVENTION: HUMAN LCCL DOMAN CONTAINING PROTEIN
                                                                                   CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: 2002-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 1123
SEQ ID NOS: 1123
SEQ ID NOS: 1123
                               FILE REFERENCE: PB0169
CURRENT APPLICATION NUMBER: US/10/060,830
CURRENT FILING DATE: 2002-01-30
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LENGTH: 17
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Matches 14; Conservative
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US-10-060-830-206
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Best Local Similarity
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Sequence 328, Application US/10339782
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynx Therapeutics, Inc.
APPLICANT: Goodman, Laurie J
APPLICANT: Bowen, Benjamin A
TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells
FILE REFERENCE: 37-0001100S
CURRENT FILING DATE: 2003-01-08
NUMBER OF SEQ ID NOS: 495
SOFTWARE: Patentin version 3.1
SEQ ID NO 328
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US-10-310-188-37271
| Sequence 37271 Application US/10310188
| SEQUENCE 37274 Application US/10310188
| TATE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY |
| TITLE OF INVENTION: USES THEREOF |
| FILE REPERENCE: 47487 |
| CURRENT APPLICATION NUMBER: US/10/310,188 |
| CURRENT PILION DATE: 2002-12-19 |
| SOFTWARE: PATENTIN OF SEQ ID NOS: 86841 |
| SOFTWARE: PATENTIN OF SEQ ID NOS: 86841 |
| SOFTWARE: PATENTIN OF SEQ ID NOS: 86841 |
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Pred. No. 5.5e+02;
0; Mismatches 1; Indels
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93.3%; Pred. No. 5.5e+02;
tive 0; Mismatches 1;
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                                    SOFTWARE: Friedman macro Napro4
SEQ ID NO 560
LENGTH: 17
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Best Local Similarity 93.3%;
Matches 14; Conservative C
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Best Local Similarity 93.34
Matches 14; Conservative
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NUMBER OF SEQ ID NOS: 4385
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; CRGANISM: Homo sapiens
US-10-310-188-37271
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                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
US-10-261-185-560
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Best Local Similarity
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Sequence 559, Application US/10261185

GENERAL INFORMATION:

APPLICANT: Kniec, Eric B.

APPLICANT: Gamper, Howard B.

APPLICANT: Rice, Michael C.

TITLE OF INVENTION: Stranded Oligonucleotides

FILE REFERENCE: NaPro-4CON

CURRENT APPLICATION NUMBER: US/10/261,185

CURRENT FILING DATE: 2002-09-27

PRIOR APPLICATION NUMBER: US 60/192,176

PRIOR PILING DATE: 2000-03-27

PRIOR FILING DATE: 2000-03-27

PRIOR FILING DATE: 2000-03-27

PRIOR FILING DATE: 2000-03-27

PRIOR FILING DATE: 2000-06-01

PRIOR PLING DATE: 2000-06-01

PRIOR PLING DATE: 2000-06-01

PRIOR PLING DATE: 2000-06-01

PRIOR PLING DATE: 2000-06-01

PRIOR FILING DATE: 2000-06-01

PRIOR PLING DATE: 2000-06-01
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JAPPILCANT: Kniec, Eric B.

APPILCANT: Gamper, Howard B.

APPILCANT: Romiec, Eric M.

APPILCANT: Rome Michael C.

TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single

TITLE OF INVENTION: Stranded Oligonucleotides

CURRENT APPLICATION NUMBER: US/10/261,185

CURRENT FILING DATE: 2001-03-27

PRIOR FILING DATE: 2000-03-27

PRIOR PILING DATE: 2000-03-27

PRIOR PILING DATE: 2000-03-27

PRIOR FILING DATE: 2000-06-01

PRIOR FILING DATE: 2000-10-30
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                                                                                                            0.6%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 5.5e+02;
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Matches 14; Conservative
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US-10-261-185-559
; ORGANISM: Homo sapiens
US-10-209-787-560
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GENERAL INFORMATION:
APPLICANT: ROLEC, ERIC B.
TITLE OF INVENTION: TARGETED NUCLEIC ACID SEQUENCE ALTERATION USING PLURAL
TITLE OF INVENTION: OLIGONUCLECATIONS
TITLE OF INVENTION: OLIGONUCLEOTIDES
TITLE OF INVENTION: OLIGONUCLEOTIDES
CURRENT APPLICATION NUMBER: US/10/623,107
CURRENT FILLING DATE: 2002-07-19
PRIOR FILLING DATE: 2002-07-19
PRIOR FILLING DATE: 2002-07-19
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GENERAL INFORMATION:
APPLICANT: KNIEC, ENC.
TITLE OF INVENTION: TARGETED NUCLEIC ACID SEQUENCE ALTERATION USING PLURAL
TITLE OF INVENTION: OLIGONUCLECTIDES
FILE REPRESENCE: NARNO-14
CURRENT APPLICATION NUMBER: US/10/623,107
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/397,555
NUMBER OF SEQ ID NOS: 7046
SEQ ID NO 560
LENGTH: 17
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93.3%; Pred. No. 5.5e+02;
tive 0; Mismatches 1; Indels
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Pred. No. 5.5e+02;
0; Mismatches 1;
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                   ; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-10-342-902-1602
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Best Local Similarity 93.33
Matches 14; Conservative
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SEQ ID NO 559
LENGTH: 17
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Best Local Similarity
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US-10-623-107-559/c
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US-10-623-107-560
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LENGTH: 17
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                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blatt, Larry
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: 400/075 (WHHB00-845-1)
CURRENT PILING DATE: 2003-01-15
FRIOR FILING DATE: 2001-06-08
FRIOR FILING DATE: 2000-03-20
FRIOR FILING DATE: 2000-03-20
FRIOR FILING DATE: 2000-06-09
FRIOR FILING DATE: 2000-10-24
FRIOR FILING DATE: 2000-10-24
FRIOR FILING DATE: 1000-09-09
FRIOR FILING DATE: 1090-01-04
FRIOR FILING DATE: 1994-02-07
FRIOR FILING DATE: 1994-02-07
FRIOR FILING DATE: 1994-02-07
FRIOR FILING DATE: 1994-02-07
FRIOR FILING DATE: 1999-11-08
FRIOR FILING DATE: 1994-02-07
FRIOR FILING DATE: 1994-03-05-14
FRIOR FILING DATE: 1999-11-08
FRIOR FILING DATE: 1994-03-05-14
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APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jun
CURRENT APPLICATION NUMBER: US/10/342,902
CURRENT APPLICATION NUMBER: US 09/877,478
PRIOR APPLICATION NUMBER: US 09/877,478
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-09-9
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 1994-02-07
PRIOR PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
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                   Sequence 909, Application US/10342902 GENERAL INFORMATION:
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; ORGANISM: Hepatitis B virus
US-10-342-902-909
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Best Local Similarity 26.7%
Matches 4; Conservative
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Sequence 559, Application US/10681074

Sequence 559, Application US/10681074

GENERAL INFORMATION:
APPLICANT: WAIK, ERIC B.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN
TITLE OF INVENTION: OLIGONUCLECTED NUCLEIC ACID SEQUENCE ALTERATION
TITLE OF INVENTION: OLIGONUCLECTED NUCLEIC ACID SEQUENCE ALTERATION
TITLE OF INVENTION: OLIGONUCLECTED NUCLEIC ACID SEQUENCE ALTERATION
CURRENT APPLICATION NUMBER: US 60/453,360
PRIOR APPLICATION NUMBER: US 60/416,983
PRIOR FILING DATE: 2003-03-07
PRIOR FILING DATE: 2003-10-07
NUMBER OF SEQ ID NOS: 4375
SOFTWARE: PATENTIN VERBION 3.2
SEQ ID NO 559
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PRIOR APPLICATION NUMBER: PCT/USO2/09187
PRIOR FILING DATE: 2002-03-26
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-0-24
PRIOR PILING DATE: 2001-10-24
PRIOR PILING DATE: 2001-10-24
PRIOR PELICATION NUMBER: US 60/359,580
PRIOR FILING DATE: 2002-02-20
PRIOR PELICATION NUMBER: US 60/369,580
PRIOR PILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR PILING DATE: 2000-03-11
PRIOR PILING DATE: 2000-03-11
PRIOR PILING DATE: 2000-03-26
PRIOR PILING DATE: 2000-02-26
PRIOR PILING DATE: 2000-02-26
PRIOR APPLICATION NUMBER: US 09/740,332
PRIOR PILING DATE: 2000-02-2-8
PRIOR PILING DATE: 2000-02-15
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93.3%; Pred. No. 5.5e+02;
Niematches 1;
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26.7%; Pred. No. 5.5e+02;
tive 10; Mismatches 1;
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; ORGANISM: Hepatitis B Virus
US-10-669-841-1602
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 4; Conserv
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US-10-681-074-559/c
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US-10-681-074-560
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TILLE OF INVENTION: OLIGONUCLECTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
TILLE OF INVENTION: OLIGONUCLECTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
TILLE OF INVENTION: OLIGONUCLECATION
FILE REFERENCE: 400/04202 (MEHBO2-249-E)
CURRENT APPLICATION NUMBER: US/10/669,841
CURRENT APPLICATION NUMBER: US/10/669,841
CURRENT APPLICATION NUMBER: US/02-03-03
PRIOR FILING DATE: 2003-09-23
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-12-05
PRIOR PRILING DATE: 2001-12-05
PRIOR FILING DATE: 2001-03-11
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-26
PRIOR PRIOR FILING DATE: 2001-03-26
PRIOR PRIOR FILING DATE: 2001-03-26
PRIOR PRIOR FILING DATE: 2001-03-26
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TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
TITLE OF INVENTION: VIRUS REPLICATION
TITLE REFERENCE: 400/042US (MBHB02-249-E)
CURRENT APPLICATION NUMBER: US/10/669,841
CURRENT FILING DATE: 2003-09-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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APPLICANT: Lawrence, Blatt
APPLICANT: Dennis, Macejak
APPLICANT: James, McSwiggen
APPLICANT: David, Morrissey
APPLICANT: Pamela, Pavco
APPLICANT: Pamela, Pavco
                                    Sequence 909, Application US/10669841 GENERAL INFORMATION:
                                                                                                          APPLICANT: Sirna Therapeutics, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  907 ATTITCTTIGGICTT 921
                                                                                                                                    Lawrence, Blatt
Dennis, Macejak
James, McSwiggen
David, Morrissey
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APPLICANT: Kenneth, Draper
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Kenneth, Draper
                                                                                                                                                                                                                                                                   Pamela, Pavco
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Best Local Similarity
Matches 4; Conserv
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                US-10-669-841-909
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APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: David K.
APPLICANT: PENN, Sharron G.
APPLICANT: RANK, David R.
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART
FILE REFERENCE: P80105
CURRENT APPLICATION NUMBER: US/10/723,361
PRIOR APPLICATION NUMBER: US/09/866,108
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLO01499
CURRENT PAPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
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PRIOR FILING DATE: 2001-05-25
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2001-01-30
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0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
Length 17;
                                                                         Indels
Query Match

0.6%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1;
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APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
FILLE REPERENCE: P80105
CURRENT APPLICATION NUMBER: US/10/723,361
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 09/866,108
PRIOR FILING DATE: 2011-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
           APPLICANT: KOHEC, ERIC B.
APPLICANT: KOHEC, ERIC B.
APPLICANT: WAN BRABANT, ANJA
APPLICANT: VAN BRABANT, ANJA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN
TITLE OF INVENTION: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION
FILE REFERENCE: Napro-18 US
CURRENT APPLICATION NUMBER: US/10/681,074
CURRENT FILING DATE: 2003-10-07
PRIOR APPLICATION NUMBER: US 60/415,983
PRIOR PLING DATE: 2002-10-07
PRIOR PLING DATE: 2002-10-07
NUMBER OF SEQ ID NOS: 4375
SOFTWARE: Parentin version 3.2
SEQ ID NO 560
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PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
REmaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 60/236,359
PRIOR PLING DATE: 2000-10-40
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
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SEQ ID NO 973
LENGTH: 17
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APPLICANT: GU, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David K.
APPLICANT: CHEN, Wensheng
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CORGANISM: Homo sapiens
US-10-681-074-560
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US-10-723-361-973
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Sequence 32, Application PC/TUS0224115
; Sequence 32, Application PC/TUS0224115
; Geglence 32, Application PC/TUS0224115
; Geglence 32, Application PC/TUS0224115
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: BALMAIN, Allan
TITLE OF INVENTION: STKIS (STKE) (GENE POLYMORPHISM AND METHODS OF DETERMINING CANC:
TITLE OF INVENTION: STKIS (STK)
CURRENT APPLICATION NUMBER: PCT/US02/24115
CURRENT APPLICATION NUMBER: US 60/334,146
PRIOR FILING DATE: 2001-11-28
PRIOR FILING DATE: 2001-11-27
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application PC/TUS0200985
GENERAL INFORMATION:
APPLICANT: Yissum Research Development Company of The Hebrew University of Jerusals
APPLICANT: Yissum Research Development Company of The Hebrew University of Jerusal
APPLICANT: Yissum Research Development Company of The Hebrew University of Jerusal
TITLE OF INVENTION: NAMOPARTICLES CONTAINING POLYMERIC NUCLEIC ACID HOWOLOGS,
TITLE OF INVENTION: PHARMACEUTICAL...
FILE REPRENSIC: 225/87
CURRENT APPLICATION NUMBER: PCT/US02/00985
CURRENT APPLICATION NUMBER: US 60/335,837
PRIOR FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
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93.3%; Pred. No. 5.8e+02;
ive 0; Mismatches 1;
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: US 09/864,761
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 1123
SOFTWARE: Agomica Sequence Listing Engine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1096 CCCACCTGGGCTTC 1110
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Best Local Similarity 93.3%;
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CRGANISM: Mus musculus
PCT-US02-00985-19
                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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PCT-US02-00985-19/c
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                                                                                                                                                                                                                                                                            SEQ ID NO 206
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LENGTH: 18
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0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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; Sequence 206 Application US/60325062
; GENERAL INFORMATION:
; APPLICANT: GM, Yizhong
APPLICANT: GM, Yizhong
; TITLE OF INVENTION: HUMAN LCCL DOMAN CONTAINING PROTEIN
; FILE REPERRICE: ADOMICA-22
CURRENT APPLICATION NUMBER: US/60/325,062
; CURRENT APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR PLILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT GU, YIZHONG
APPLICANT: GL, YIZHONG
APPLICANT: GL, YIZHONG
TITLE OF INVENTION: HUMAN LCCL_DOMAN CONTAINING PROTEIN
FILE REFERENCE: AEOMICA-22
CURRENT APPLICATION: HUMAN LCCL_DOMAN CONTAINING PROTEIN
CURRENT FILING DATE: 2001-09-25
PRIOR PELLING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: US 09/864,761
PRIOR PILING DATE: 2001-01-30
  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 73370 LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 203, Application US/60325062 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     1133 TCACCTCCAGCTCCA 1147
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Best Local Similarity 93.3
Matches 14; Conservative
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SOFTWARE: Aeomica Sequence
SEQ ID NO 203
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CORGANISM: Homo sapiens
US-60-325-062-203
                                                                                                              ; ORGANISM: Homo sapiens
US-10-741-600-73370
                                                                                       TYPE: DNA
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APPLICANT: Yissum Research Development Company of The Hebrew University of Jerusale APPLICANT: Yissum Research Development Company of The Hebrew University of Jerusal TITLE OF INVENTION: ANONPARTICLES CONTAINING FOLYMERIC NUCLEIC ACID HOMOLOGS, TITLE OF INVENTION: PHARMACEUTICAL...
FILE REFERENCE: 325/87
CURRENT APPLICATION NUMBER: PCT/ILO2/00985
CURRENT APPLICATION NUMBER: DC 60/335,837
PRIOR APPLICATION NUMBER: US 60/335,837
NUMBER OF SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: IDENTIFYING AND CHARACTERIZING HEPATITIS C
FILE REFERENCE: PCV-OUPC
CURRENT APPLICATION NUMBER: PCT/US03/07585
CURRENT APPLICATION NUMBER: PCT/US03/07585
PRIOR FILING DATE: 2002-03-03-11
PRIOR FILING DATE: 2002-03-11
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FASLEED for Windows Version 4.0
SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                         Length 18;
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                                                                                                                                                                                                                                                                                                                                       Score 13.4; DB 1;
Pred. No. 5.8e+02;
0; Mismatches 1;
PRIOR APPLICATION NUMBER: US 60/337,052
PRIOR FILING DATE: 2001-12-04
PRIOR PILING DATE: 2002-03-28
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 564
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 162
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US03-07585-40; Sequence 40, Application PC/TUS0307585; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                         0.68;
                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                       14; Conservative
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                                                                                                                                                                                                                                          FEATURE:
CTHER INFORMATION: Primer
PCT-US02-34679-162
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Best Local Similarity
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LENGTH: 18
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APPLICANT: Bertram, Lars
APPLICANT: Saunders, Aleister J.
APPLICANT: Munit, Katistina M.
APPLICANT: Sampson, Andrew Johnson
APPLICANT: Blacker, Deborah Lynne
APPLICANT: Blacker, Deborah Lynne
APPLICANT: Blacker, Deborah Lynne
TITLE OF INVENTION: GENES AND FOLYMORPHISMS ON CHROMOSOME 10
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
TITLE OF INVENTION: NUMBER: PCT/US02/34679
CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: US 60/339,525
PRIOR APPLICATION NUMBER: US 60/339,010
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/336,929
PRIOR APPLICATION NUMBER: US 60/338,363
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/338,363
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TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmi
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PCT/US02/25940
CURRENT APPLICATION NUMBER: 2002-08-27
NUMBER OF SEQ ID NOS: 25502
SOFTWARE: Proprietary
SEQ ID NO 18207
LENGTH: 18
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ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmi
                                                                                                                                                                   Length 18;
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0.6%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1;
                                                                                          CTHER INFORMATION: Amplification reaction primer PCT-US02-24115-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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PCT-00202-34679-162/C
Sequence 162, Application PC/TUS0234679
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Tanzi, Kathryn J.
; APPLICANT: Tanzi, Tuscker.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 18207, Application PC/TUS0225940; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                              1093 ACCCCCACCCTGGGC 1107
                    TYPE: DNA
ORGANISM: Artificial sequence
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Matches 14; Conservative
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APPLICANT:
APPLICANT:
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APPLICANT: STUYVER,
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ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-OCC-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION: ALMKNOWN>
PRIOR APPLICATION DATA:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SUTVYUR, LIEVEN
ROSSAU, RUDI
MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 18;
                                    0.6%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 5.8e+02; tive 0; Mismatches 1; Indels
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93.3%; Pred. No. 5.8e+02;
ative 0; Mismatches 1;
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FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE, DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 270:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 907
US-09-155-885A-272/c
Sequence 272, Application US/09155885A
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEG ID NO: 270:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                        1096 CCCACCCTGGGCTTC 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 728 GCCAGGAGAACAGA 742
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                                                                                                                                                            cccaccardedcrire 3
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                                    Query Match
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-155-885A-270
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Best Local Simi
Matches 14;
  PCT-IL02-00985-19
                                                                                                                                                               17
                                                                                                                                                                                                                             RESULT 906
US-09-155-6
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                                                                                                                                                                                                                                                                      SITEM: 1100 NORTH GLESE KOAD
CITY: ARLINOTON
STATE: VIRGINIA
COUNTRY: 0.5.A.

ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
CLASSIFICATION NUMBER: PC-1998
FILING DATE: 12-ARV-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 13-ARV-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
THE TELECOMMUNICATION INFORMATION:
THE TELECOMMUNICATION I
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ROSSAU, RUDI
MARRIERS, GEBRY
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 18;
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) Sequence 273, Application US/09155885A
; GENERAL INFORMATION:
    APPLICANT: STUYVER, LIEVEN
; MARRIENS, GERRT
; TITLE OF INVENTION:
    NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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93.3%; Pred. No. 5.8e+02;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 272:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703) 816-4:
INFORMATION FOR SEQ ID NO: 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: VIRGINIA COUNTRY: U.S.A.
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Sequence 47, Application US/10108732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 rcaccrecaecreca 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCCTCACCCTGGGC
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Sequence 18, Application US/09857278

GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Elex M. Cowsert
ITILE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
CURRENT FILING DATE: 2001-06-01
PRIOR PPLICATION NUMBER: US/09/857,278
CURRENT APPLICATION NUMBER: 09/205,204
PRIOR FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 47
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
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O.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.6%; Score 13.4; DB 1; Length 18; Best Local Similarity 93.3%; Pred. No. 5.8e+02; Matches 14; Conservative 0; Mismatches 1; Indels
                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-0ct-1938
CLASSIFICATION NUMBER: US/09/155,885A
FILING DATE: 21-APPLICATION
FILING DATE: 21-APR-1937
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 21-APR-1966
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (703) 816-4000
TELEFRAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 273:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 273:
US-09-155-885A-273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             761 ATGCAGGTTTCTTTC 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Synthetic US-09-857-278-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 ArGCAGGCTTCTTTC 18
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Matches
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RESULT 910 US-10-108-732-47/c

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Sequence 32, Application US/10209324
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF CALLFORNIA SAN FRANCISCO
APPLICANT: UNIVERSITY OF CALLFORNIA SAN FRANCISCO
APPLICANT: UNIVERSITY OF CALLFORNIA SAN FRANCISCO
TITLE OF INVENTION: STX15 (STK6) GENE POLYMORPHISM AND METHODS OF DETERMINING CANCI
FILE REFERENCE: USF1120-2
CURRENT PELLOGATION NUMBER: US/10/209,324
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US 60/334,146
PRIOR APPLICATION NUMBER: US 60/334,146
PRIOR FILING DATE: 2001-11-28
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
SEQ ID NO 32
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: hMSHR C-inner sequencing primer 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

0.6%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.6%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , CTHER INFORMATION: Amplification reaction primer US-10-209-324-32
APPLICANT: Box, Neil F
APPLICANT: Box, Neil F
APPLICANT: Box, Neil F
APPLICANT: Box, Neil F
APPLICANT: Bayward, Nicholas K
APPLICANT: Sturm, Nicholas G
APPLICANT: Sturm, Nicholas G
APPLICANT: Gruis, Neileke A
APPLICANT: Bergman, Wilms
APPLICANT: Bergman, Wilms
APPLICANT: Frants, Rune R
CURRENT FAILNG DATE: 2002-03-28
FRICR APPLICATION NUMBER: US 60/279,515
FRICR APPLICATION NUMBER: US 60/279,515
FRICR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 76
SECTWARE: Patentin version 3.1
LENGTH: 18
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; Sequence 18207, Application US/10227563
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APPLICANT: RosettaGemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION UNMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
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0
                                                                                                                                                                                      APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Helicobacter pylori 26695 complete genome.
FILE REFRENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/294,040
CURRENT FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1102
SOFTWARE: Proprietary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TILLE OF INVENTION: Helicobacter pylori 26695 complete genome.
FILE REPERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/294,040
CURRENT FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1102
SOFTWARE: Proprietary
SEQ ID NO 279
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 5.8e+02; ive 0; Mismatches 1; Indels
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; OTHER INFORMATION: Chromosome = 1 Strand = positive US-10-294-040-279
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Helicobacter pylori 26695 complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Helicobacter pylori 26695 complete genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 279, Application US/10294040; GENERAL INFORMATION:
                                                                                                                                               Sequence 54, Application US/10294040 GENERAL INFORMATION:
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16 AGAGAAGCCTGGAGT 2
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Matches 14; Conservative
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LENGTH: 18
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APPLICANT: Sampson, Andrew Johnson
APPLICANT: Blacker, Deborah Lynne
TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE
TITLE OF INVENTION: HURODEGENERATIVE DISEASES
FILE REFERRACE: 37481-3308
CURRENT PELLING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: US 60/339,525
PRIOR APPLICATION NUMBER: US 60/339,010
PRIOR PELLING DATE: 2001-11-08
PRIOR PELLOR DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/336,929
PRIOR APPLICATION NUMBER: US 60/336,929
PRIOR PELLING DATE: 2001-11-08
PRIOR PELLING DATE: 2001-12-04
PRIOR PELLING DATE: 2001-12-04
PRIOR PELLING DATE: 2001-32-8
NUMBER OF SEQ ID NOS: 564
SOFTWARE: PRESENCE FOR WINDOWN VETRION 14.0
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                 APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmi
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/227,563
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 25502
SOFTWARE: Proprietary
SEQ ID NO 18207
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 13.4; DB 1; Length 18; larity 93.3%; Pred. No. 5.8e+02; Conservative 0; Mismatches 1; Indels
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93.3%; Pred. No. 5.8e+02;
cive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 162, Application US/10282174 GENERAL INFORMATION:
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Saunders, Aleister J.
Mullin, Kristina M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Becker, Kenneth David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Velicelebi, Gonul
Elliot, Kathryn J.
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Best Local Similarity 93.34
Matches 14; Conservative
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Best Local Similarity
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APPLICANT:
APPLICANT:
APPLICANT:
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STREET: 1100 NORTH GLEBE ROAD
CITY: ALLINGTON
STREET: 1100 NORTH GLEBE ROAD
CITY: ALLINGTON
STREET: VIRGINIA
COMPUTE: VIRGINIA
COMPUTER READABLE FORM
COMPUTER READABLE FORM
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            MAERTENS, GEERT TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV NUMBER OF SEQUENCES: 313 CORRESPONDENCE ADDRESS:
                                              Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 18;
                                                                                                Indels
                                            0.6%; Score 13.4; DB 1;
33.3%; Pred. No. 5.8e+02;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.6%; Score 13.4; DB 1;
33.3%; Pred. No. 5.8e+02;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
BLING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/155,885A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: SALOOF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 270:
                                                                                                                                                                                                                                                                                                          Sequence 270, Application US/10453792
GENERAL INFORMATION:
APPLICANT: SIUVYER, LIEVEN
ROSSAU, RUDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                       93.38;
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                                                                                             14; Conservative
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                                                 Query Match
Best Local Similarity
Matches 14; Conserv
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US-10-453-792-272/c
                                                                                                                                                                                                                                                                RESULT 919
US-10-453-792-270/c
    US-10-367-892-18207
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ORGANIEM: Deinococcus radiodurans R1 complete genome, Plasmi
FEATURE:
LOCATION: (2199746)...(2199763)
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 21297
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APPLICANT: Cohen, Daniel
APPLICANT: COHen, Daniel
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
TITLE CALUMAKOV, 11ya
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/10/349,143
CURRENT APPLICATION NUMBER: US/09/422,978
PRIOR PILING DATE: 1999-00-20
PRIOR PILING DATE: BARLIER APPLICATION NUMBER: US 60/298,850
PRIOR PILING DATE: BARLIER APPLICATION NUMBER: US 60/109,732
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
PRIOR PILING DATE: BARLIER FILING DATE: 1999-11-23
PRIOR FILING DATE: BARLIER FILING DATE: 1998-11-23
PRIOR FILING DATE: BARLIER FILING DATE: 1998-04-21
PRIOR FILING DATE: BARLIER APPLICATION NUMBER: US 60/082,614
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO SOSS
LENGTH: 18
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; OTHER INFORMATION: upstream amplification primer 99-20747 for SEQ 1151, US-10-349-143-5085
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TITLE OF INVENTION: Delinococus radiodurans R1 complete genome, Plasmi
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/367,892
CURRENT FILING DATE: 2003-03-06
NUMBER OF SEQ ID NOS: 25502
SEQ ID NO 18207
LENGTH: 18
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                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                  Indels
                                                                                                                                                                   Query Match 0.6%; Score 13.4; DB 1; Best Local Similarity 93.3%; Pred. No. 5.8e+02; Matches 14; Conservative 0; Mismatches 1;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 82210
LENGTH: 18
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                                                                                                                                                                                                                                                                967 CGGTGGAAGTCCAAG 981
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US-10-310-188-82210
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Best Local Similarity
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                                                                          TYPE: DNA
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Matches
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Sequence 18, Application US/10464158

GENERAL INFORMATION:
TOWNERL INFORMATION:
TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-1
TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-1
TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-1
TITLE OF INVENTION: ANDIBER: US/10/464,158
CURRENT APPLICATION NUMBER: US/10/464,158
FRIOR PELING DATE: 2003-06-18
FRIOR PELING DATE: 2003-06-18
FRIOR FILING DATE: 1999-06-16
FRIOR FILING DATE: 1999-06-16
FRIOR FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 48
FRIOR FILING DATE: 1998-12-03
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0
      COMPUTER READABLE FORM:
COMPUTER: FIORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 5.8e+02; Live 0; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.6%; Score 13.4; DB 1;
93.3%; Pred. No. 5.8e+02;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                   PRILING DATE: 04/Un-2003

CLASSIFICATION: (Unknown)

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

FILING DATE: 08-Oct-1998

APPLICATION NUMBER: PCT/EP97/02002

FILING DATE: 21-APR-1997

APPLICATION NUMBER: EP 96870053.4

FILING DATE: 19-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B.J.

REGISTRATION NUMBER: 36,663

REFRENCE/DOCKET NUMBER: 2551-5

TELEPHONE: (703) 816-4100

TELEPHONE: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Antisense Oligonucleotide US-10-464-158-18
                                                                                                                                                                                                                   APPLICATION NUMBER: US/10/453,792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO SEQUENCE DESCRIPTION: SEQ ID NO: 273: US-1C-453-792-273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 273: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              728 GCCAGGAGAACAGA 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 GCCAGGAGAAACGGA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 93.33
Matches 14, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.6
Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                       STATE: VIRGINIA
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION: «Unknown»
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TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 5.8e+02; tive 0; Mismatches 1; Indels
                                                                                                         MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-00c-1998
APPLICATION NUMBER: PCT/FE97/02002
FILING DATE: 21-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
                                                                                                                                                                                                                                            ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 272:
US-10-453-792-272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: SADOFF, B.J.
REGISTRATION UNDRER: 36,663
REFERENCE/DOCKET UNDRER: 2551-5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 273, Application US/10453792 GENERAL INFORMATION:
Sequence 272, Application US/10453792
GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (703) 816-4000 TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 272:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                728 GCCAGGAGAACAGA 742
                                                                                          RUDI
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Best Local Similarity 93.3
Matches 14; Conservative
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RESULT 925
US-10-606-879-272/c
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APPLICANT: Bertram, Lars
APPLICANT: Saunders, Aleister J.
APPLICANT: Blacker, Deborah Lynne
TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE
TITLE OF INVENTION: ASSOCIATED WIGHER: US/10/600,009
TITLE OF INVENTION: NUMBER: US 60/339,525
PRIOR PELLING DATE: 2001-11-08
PRIOR PELLING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/336,363
PRIOR PELLING DATE: 2001-11-08
PRIOR PELLING DATE: 2001-11-08
PRIOR PELLING DATE: 2001-12-04
PRIOR PELLING DATE: 2001-12-04
PRIOR PELLING DATE: 2001-12-04
PRIOR PELLING DATE: 2001-12-04
PRIOR PELLING DATE: 2002-03-28
PRIOR PELLING DATE: 2002-03-28
PRIOR PELLING DATE: 2002-03-28
PRIOR PELLING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 564
SEQ ID NO 162
LENGTH: 18
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TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 5.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 270, Application US/10606879
GENERAL INFORMATION:
APPLICANT: STUTYER, LIEVEN
ROSSAU, RUDI
                                                                                                                                                          Sequence 162, Application US/10600009 GENERAL INFORMATION:
                                                                                                                                                                                                         APPLICANT: Becker, Kenneth David
APPLICANT: Velicelebi, Gonul
APPLICANT: Elliot, Kathryn J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
761 ATGCAGGTTTCTTTC 775
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                                                                                                                                                                                                                                                                                    Wang, Xin
Tanzi, Rudolph E.
                                               4 ATGCAGGCTTCTTTC 18
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hes 14; Conservative
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US-10-606-879-270/c
                                                                                                                                        -10-600-009-162/c
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Matches
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Gaps
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ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE SIDENSES:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 13.4; DB 1; 93.3%; Pred. No. 5.8e+02;
                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-0ct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/606,879
FILING DATE: 27-Jun-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/606,879
FILING DATE: 27-Jun-2003
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO
ANTI-SBNSE: NO
SAUTHORN DESCRIPTION: SEQ ID NO: 270:
US-10-606-879-270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 272, Application US/10606879
GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDENDESS: aingle
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 270: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     728 GCCAGGAGAAACAGA 742
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Best Local Similarity
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APPLICANT: Brenda F. Baker
APPLICANT: Brenda F. Baker
APPLICANT: Timothy Vickers
APPLICANT: Timothy Vickers
APPLICANT: C. Frank Benner
APPLICANT: Susan M. Ereier
TITLE OF INVENTION: OLIGOMERIC COMPOUNDS AND COMPOSITIONS FOR USE IN MODULATION OF
FILE REFERENCE: COREOLOGUS.L
CURRENT APPLICATION NUMBER: US/60/492,056
URRENT FILING DATE: 2003-08-13
NUMBER OF SEQ ID NOS: 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Chumackov, Ilya
APPLICANT: Chumackov, Ilya
APPLICANT: Abderrahim, Hadi
APPLICANT: Dufaure-Gare, Isabelle
TITLE OF INVENTION: BIALLELIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY.
FILE REPERBENCE: 84.US1.PRO
CURRENT APPLICATION NUMBER: US/60/216,745
UNMBER OF SEQ ID NOS: 13665
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; OTHER INFORMATION: upstream amplification primer 99-53687 for SEQ 3688,
US-60-216-745-8219
                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 5.8e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                       Query Match

0.6%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1;
                                                                                                                                                               ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 273:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FASTSEQ for Windows Version 4.0 SEQ ID NO 743 LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-60-216-745-8219/c; Sequence 8219, Application US/60216745; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 743, Application US/60492056; GENERAL INFORMATION:
                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                          LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

Best Local Similarity 93.3%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             18 GCCAGGAGAAACGGA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo Sapiens
                                                                                                                                          HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: primer_bind
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SEQ ID NO 8219
LENGTH: 18
                                                                                                                                                                                                            US-10-606-879-273
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COUNTRY: U.S.A.
ZIPE 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 273, Application US/10606879
GENERAL INFORMATION:
APPLICANT: STUTVER, LIEVEN
MAERIENS, GERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 5.8e+02; ative 0; Mismatches 1; Indels
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FILING DATE: 27-Jun-2003
CLASSIFICATION NUMBER: US/10/606,879
FILING DATE: 27-Jun-2003
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 119-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION:
FILING DATE: 08-Oct-1998
APPLICATION NUBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 2551-5
TELEFRENCE/DOCKET NUMBER: 2551-5
TELEFAN: (703) 816-4100
INFORMATION FOR SEQ ID NO: 272:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 272:
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TELEPHONE: (703) 816-4000
INFORMATION FOR SEQ ID NO: 273:
                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  728 GCCAGGAGAACAGA 742
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Best Local Similarity 93.3
Matches 14; Conservative
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Bejeglman, Leonid
APPLICANT: Bejeglman, Leonid
APPLICANT: Chowrita, Bharat
TITLE OF INVENTION: Factor (FDGF) and Platelet Derived Growth Factor Receptor (FDC
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
FILE REFERENCE: 03-073 (400/092)
FRICK APPLICATION NUMBER: US 60/363,124
FRICK APPLICATION NUMBER: US 60/363,124
FRICK FILING DATE: 2002-03-11
FRICK FILING DATE: 2002-09-05
FRICK APPLICATION NUMBER: US 60/409,293
FRICK FILING DATE: 2002-09-05
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; Sequence 178, Application PC/TUS0303662
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leonid
; APPLICANT: Thompson, James
; APPLICANT: Thompson, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Cyclin D1 Gene Express:
                                                                                                                                                                                                             Target Sequence/siNA sense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region PCT-US03-03473-352
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                                                                                                                                                                                                                                                                               Score 13.4; DB 1; Length 1:
Pred. No. 6e+02;
                                                                                                                                                            ; FEATURE;
; OTHER INFORMATION: Description of Artificial Sequence:
PCT-USO3-03473-41
                                                                                                                                                                                                                                                                                           0.6%; Scor.
73.3%; Pred. No. ec.
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PCT-US03-03473-352/c
; Sequence 352, Application PC/TUS0303473
; GENERAL INFORMATION:
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                                         LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
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SOFTWARE: Patentin version 3.2
SEQ ID NO 352
LENGTH: 19
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ORGANISM: Artificial Sequence
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Best Local Similarity 73.3%
Matches 11; Conservative
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                SEQ ID NO 41
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Decorporation in the constant of the co
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GENERAL INFORMATION:
APPLICAMY: KARLSEN, FRANK
TITLE OF INVENTION: ONTAMINATION IN SAMPLES
FILE REPRESENCE: 618123-6
CURRENT APPLICATION NUMBER: PCT/US00/22029
PRIOR PEPILAGATION NUMBER: PCT/US00/22029
PRIOR APPLICATION NUMBER: 60/149,365
PRIOR FILING DATE: 1999-08-13
NUMBER: OF SEQ ID NOS: 38
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                                                                                                                                                                                                         Length 18;
                                                                                                                                                                                                                                                                               Indels
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0.6%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1;
                                                                         OTHER INFORMATION: Antisense Oligonucleotide
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PRIOR FILING DATE: 2003-01-15
WUMBER OF SEQ ID NOS: 672
SOFTWARE: Patentin version 3.2
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                         887 CAGIGCIGITGCCCC 901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US00-22029-11/c
                                                                                                                   US-60-492-056-743
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                                    FEATURE
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GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwiggen, James

APPLICANT: McSwiggen, Jemes

APPLICANT: Bejeglaman, Leonid

TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)

TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)

TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)

TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)

TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)

TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)

FRIOR PELICATION NUMBER: US 60/356,905

PRIOR PELING DATE: 2002-03-11

PRIOR PELING DATE: 2002-03-11

PRIOR PELING DATE: 2002-06-06

PRIOR PELING DATE: 2002-06-06

PRIOR PELING DATE: 2002-09-05

PRIOR PELING DATE: 2003-09-05

PRIOR PELING
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PCT-US03-04908-231
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; Sequence 645, Application PC/TUS0304908
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: Using Short Interfering Nucleic Acid (sina)
; FILE REPERBNCE: 02-714-A (400/086)
; CHRRENT APPLICATION NUMBER: PCT/US03/04908
; CURRENT FILING DATE: 2003-02-18
                                                                                                  FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region PCT-US03-03662-417
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                                                                                                                                                                                                                                                                                     1; Indels
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0.6%; Score 13.4; DB 1;
Best Local Similarity 80.0%; Pred. No. 6e+02;
Matches 12; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                       Score 13.4; DB 1;
Pred. No. 6e+02;
                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US03-04908-231
; Sequence 231, Application PC/TUS0304908
; GENERAL INFORMATION:
                                                                                                                                                                                                                       Query Match 0.6%; Sc
Best Local Similarity 80.0%; Pr
Matches 12; Conservative 2;
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SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA
ORGANISM: Artificial Sequence
                                                                    ORGANISM: Artificial Sequence
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GENERAL INFORMATION
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Reiselman, Leonid
APPLICANT: Reiselman, Leonid
APPLICANT: Thompson, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Cyclin DI Gene Expression
TITLE OF INVENTION: Wing Short Interfering Nucleic Acid (sina)
TITLE OF INVENTION: Wing Short Interfering Nucleic Acid (sina)
TITLE OF INVENTION: USing Short Interfering Nucleic Acid (sina)
TITLE OF INVENTION NUMBER: US 60/411,275
PRIOR PLILOR DATE: 2002-02-20
PRIOR FILING DATE: 2002-02-17
PRIOR PLILOR DATE: 2002-03-11
PRIOR PLILOR DATE: 2002-03-11
PRIOR PLILOR DATE: 2002-03-11
PRIOR PLILOR DATE: 2002-06-06
PRIOR PLILOR DATE: 2002-06-06
PRIOR FILING DATE: 2002-09-05
PRIOR FILING DATE: 2002-09-09
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 530
SOFTWARE: PatentIn version 3.2
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FILE REFERENCE: 02-1005-A (400/083)
CURRENT APPLICATION NUMBER: PCT/US03/03662
CURRENT FILING DATE: 2003-02-06
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0; Mismatches
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Matches 14; Conserv
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LENGTH: 19
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SOFFWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,620
FILING DATE: 06-NOV-1997
                                                                                                                                                                                                 6e+02;
                                                                                                                                                                          Score 13.4; D
Pred. No. 6e+0
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 775, Application US/08965620
GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Hudson, Thomas
TITLE OF INVENTION: Biallelic Markers
INDER OF SEQUENCES: 3817
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & RE
       SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 06-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 60/030,455
FILING DATE: 06-NOV-1996
ATTORNEY/ACENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 939
18-09-634-960A-11/c
Sequence 11, Application US/09634960A
GENERAL INFORMATION:
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TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
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REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                 cacadrecirridec 1
                                                                                                                                                                     Query Match 0.63
Best Local Similarity 93.33
Matches 14; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
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STRANDEDNESS: single
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                                                                                       ORGANISM: Homo sapiens
PCT-USQ3-40978-73310
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Best Local Similarity
Matches 14; Conserv
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US-08-965-620-775/c
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ZIP: 02173
                           SEQ ID NO 73310
LENGIH: 19
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                                                                             TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: PCT/US03/40978
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Description of Artificial Sequence: sinA antisense region PCT-US03-04908-645
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GENERAL INFORMATION:
APPLICAMY: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001500
CURRENT APPLIANCION NUMBER: PCT/US03/40977
CURRENT PILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOPTWARE: PARESEQ for Windows Version 4.0
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               PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: US 60/359,580
PRIOR PILING DATE: 2002-02-0
PRIOR PILING DATE: 2002-03-11
PRIOR PILING DATE: 2002-03-11
PRIOR FILING DATE: 2002-03-11
PRIOR PILING DATE: 2002-06-06
PRIOR PILING DATE: 2002-06-06
PRIOR PILING DATE: 2002-06-09
PRIOR PILING DATE: 2002-09-09
PRIOR FILING DATE: 2002-09-09
PRIOR FILING DATE: 2002-09-09
PRIOR PILING DATE: 2003-09-09
PRIOR PILING DATE: 2003-01-15
US 60/396,905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
ORGANISM: Artificial Sequence
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Matches 14; Conservative
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CRGANISM: HOMO Sapiens
PCT-US03-40977-26190
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Sequence 637, Application US/10244647
GENERAL INFORMATION:
APPLICANT: Biozyme Pharmaceutical, Inc.
APPLICANT: McEviggen, James
APPLICANT: McEviggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: Short Interfering Nucleic Acid (sinA)
TITLE OF INVENTION: Short Interfering Nucleic Acid (sinA)
FILE REFERENCE: 400/060 (WBHB02-1000)
CURRENT APPLICATION NUMBER: US/10/244,647
CURRENT FILING DATE: 2003-04-14
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: Patentin version 3.0
SEQ ID NO 637
SEQ ID NO 637
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-244-647-598
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US-10-244-647-637
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O.6%; Score 13.4; DB 1;
Best Local Similarity 26.7%; Pred. No. 6e+02;
Matches 4; Conservative 10; Mismatches 1;
                             CURRENT FILING DATE: 2003-04-14

PRIOR APPLICATION NUMBER: US 60/358,580

PRIOR FILING DATE: 2002-02-20

PRIOR FILING DATE: 2002-07-03

PRIOR FILING DATE: 2002-07-03

PRIOR APPLICATION NUMBER: PCT US02/09187

PRIOR APPLICATION NUMBER: PCT US02/09187

PRIOR FILING DATE: 2002-03-26

PRIOR FILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 1524

SEQ ID NO 598

LENGTH: 19
             CURRENT APPLICATION NUMBER: US/10/244,647
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                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                   TYPE: RNA
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APPLICANT: Karlsen, Frank
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF THE INDICATORS OF CONTAMINATION IN 1
TITLE OF INVENTION: SAMPLES
FILE REPERENCE: 5775.018
CURRENT APPLICATION NUMBER: US/09/634,960A
CURRENT FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/149,365
PRIOR APPLICATION NUMBER: 60/149,365
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
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APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
TITLE OF INVENTION: Short Interfering Nucleic Acid (sinA)
FILE REFERENCE: 400/060 (MBHB02-1000)
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APPLICANT: WIALER, Gerhard
APPLICANT: SLADE, Martin Basil
APPLICANT: WILLIARS, Keith Leslie
APPLICANT: WILLIARS, Keith Leslie
APPLICANT: GOOLEY, Andrew Arthur
APPLICANT: GOOLEY, Andrew Arthur
APPLICANT: Macquarie Research Ltd
TITLE OF INVENTION: CYPQUESPORIGHUM SPOROZOİTE ANTIGENS;
CURRENT APPLICATION NUMBER: US/10/148,687
CURRENT APPLICATION NUMBER: PCT/AUGO/01492
PRIOR PILING DATE: 2000-12-01
PRIOR PILING DATE: 2000-12-01
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 67
SOOTHARE: PATENTIN VET. 2.1
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceutical, Inc.
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Sequence 55, Application US/10148687
GENERAL INFORMATION:
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Best Local Similarity 93.3
Matches 14; Conservative
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US-09-634-960A-11
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Best Local Similarity
Matches 14; Conserv
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LENGTH: 19
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LENGTH: 19
                                                                                                                                                                                                                                                                                                         TYPE: DNA
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Sequence 2823, Application US/10293338
GENERAL INFORMATION:
APPLICANT: ROSettadenomics LTD
TITLE OF INVENTION: THEREOF
FILE RFFERENCE: 45282
CURRENT APPLICATION UNMERR: US/10/293,338
CURRENT FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 8785
SSOFTWARE: Patentin version 3.1
LENGTH: 19
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GENERAL INFORMATION:
APPLICANT: ROSettaGenomics LTD
TITLE OF INVENTION: PIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AN
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 45282
CURRENT APPLICATION NUMBER: US/10/293,338
CURRENT PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 8785
SOFTWARE: Patentin version 3.1
SEQ ID NO 3206
LENGTH: 19
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
CURRENT PELICATION NUMBER: US/10/303,778
CURRENT PELING DATION NUMBER: 2002-11-26
NUMBER OF SEQ ID NOS: 17608
SOFTWARE: Patentin version 3.1
SEQ ID NO 6522
LENGTH: 19
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Pred. No. 6e+02;
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33.3%; Pred. No. 6e+02;
ive 0; Mismatches 1;
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6e+02;
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Matches 14; Conservative (
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               15 ATTTTCTTTTGTCTT 1
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Best Local Similarity 93.3
Matches 14; Conservative
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ORGANISM: Homo sapiens
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                                                                                   RESULT 945
US-10-293-338-2823/c
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                 APPLICANT: MCSWigger, David
APPLICANT: MCSWigger, David
APPLICANT: MCSWigger, David
APPLICANT: McSwigger, James
APPLICANT: McSwigger, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U
TITLE OF INVENTION: Short Interfering Nucleic Acid (siNA)
TITLE OF INVENTION: Short Interfering Nucleic Acid (siNA)
TITLE OF INVENTION: Short Interfering Nucleic Acid (siNA)
TITLE OF INVENTION: Short Interfering Number: US/10/244,647
CURRENT APPLICATION NUMBER: US 60/358,580
PRIOR PILING DATE: 2002-02-20
PRIOR PILING DATE: 2002-03-26
PRIOR PLICATION NUMBER: US 60/394,876
PRIOR PILING DATE: 2001-06-08
PRIOR PILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
SEQ ID NO: 1524
SEQ ID NO: 1244
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APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morrissey, David
APPLICANT: Morrissey, David
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Short Interfering Nucleic Acid (sinA)
TITLE OF INVENTION: Short Interfering Nucleic Acid (sinA)
FILE REFERENCE: 400/060 (MBHBO2-1000)
CURRENT FILING DATE: 2003-04-14
CURRENT FILING DATE: 2002-02-20
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-03-26
PRIOR FILING DATE: 2002-03-26
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: PatentIn version 3.0
LENGTH: 19
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OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region US-10-244-647-1244
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0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
APPLICANT: Ribozyme Pharmaceutical, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 944
US-10-244-647-1283/c
; Sequence 1283, Application US/10244647
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-10-310-188-72707

Sequence 72707, Application US/10310188

Sequence 72707, Application US/10310188

Sequence 72707, Application US/10310188

APPLICANT: ROSELIAGEMONICS

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION UNMBER: US/10/310,188

CURRENT FILING DATE: 2002-12-19

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: Patentin version 3.1

SEQ ID NO 72707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 59914, Application US/10310188
GENERAL INFORMATION:
APPLICATE ROSELEGGEMOID.
TITLE OF INVENTION: BLOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT PILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SCOTWARET PLANTED APPLICATION NUMBER: US/10/310,188
SEQ ID NO S9914
ILENGTH: 19
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    CURRENT APPLICATION NUMBER: US/10/310,188 CURRENT FILING DATE: 2002-12-19 NUMBER OF EEQ ID NOS: 86841 SOFTWARE: Patentin version 3.1 SEQ ID NO 21659
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Matches 14, Conservative
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                                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-10-310-188-21659
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ORGANISM: Homo sapiens
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Best Local Similarity
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Best Local Similarity
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 9763
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Sequence 21659, Application US/10310188
GENERAL INFORMATION:
APPLICANT: RosettaGemonics
TITLE OF INVENTION: BIGINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: 47487
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GENERAL INFORMATION:
APPLICANT: ROSECTEGENOMICS
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
FILE REFERENCE: 47416
CURRENT APPLICATION NUMBER: US/10/303,778
CURRENT FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 17608
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1820
LENGTH: 19
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                                            0.6%; Score 13.4; DB 1; Length 19; 93.3%; Pred. No. 6e+02; tive 0; Mismatches 1; Indels
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93.3%; Pred. No. 6e+02;
Live 0; Mismatches 1; Indels
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                                       Query Match
Best Local Similarity 93.3
Matches 14; Conservative
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Best Local Similarity 93.3
Matches 14; Conservative
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US-10-310-188-9763
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Best Local Similarity
Matches 14; Conserv
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US-10-303-778-6522
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Sequence 73310, Application US/10741600
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 73310
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GENERAL INFORMATION:
APPLICAMT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC FOLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC FOLYMORPHISMS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741, 601
CURRENT FILING DATE: 2083-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FASISEQ for Windows Version 4.0
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93.3%; Pred. No. 6e+02;
tive 0; Mismatches 1;
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33.3%; Pred. No. 6e+02;
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Pred. No. 6e+02;
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              CURRENT APPLICATION NUMBER: US/10/707,147
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 20189
SEQ ID NO 1738
LENGTH: 19
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Matches 14; Conservative
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US-10-707-147-1738
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FILE REFERENCE: 49992
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Best Local Similarity
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Best Local Similarity
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US-10-741-600-73310/c
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US-10-741-601-26190/c
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Matches
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GENERAL INFORMATION:
SPELICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
TITLE OF INVENTION: USES THEREOF
                                                                   APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, 11ya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET 020CP1
CURRENT APPLICATION NOMBER: US/09/422,978
PRIOR APPLICATION NUMBER: BALLIER APPLICATION NUMBER: US 09/298,850
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-11-23
PRIOR PLING DATE: EARLIER FILING DATE: 1998-04-21
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
SEQ ID NO 7262
LENGTH:: 19
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VACCINIA REGULATORY
TITLE OF INVENTION: GENES AND USES THEREOF
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; OTHER INFORMATION: upstream amplification primer 99-3335 for SEQ 3328,
US-10-349-143-7262
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0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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33.3%; Pred. No. 6e+02;
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Best Local Similarity 93.3%; Pred. No. 6e+0
Matches 14; Conservative 0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/605,840
CURRENT FILING DATE: 2003-10-30
NUMBER OF SEQ ID NOS: 3750
SOFTWARE: Patentin version 3.2
SEQ ID NO 3515
                                 Sequence 7262, Application US/10349143 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3515, Application US/10605840 GENERAL INFORMATION:
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FEATURE:
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; ORGANISM: Homo sapiens
US-10-605-840-3515
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         US-10-349-143-7262/c
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CTHER INFORMATION: Antisense Oligonucleotide Us-10-317-277A-67
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                      STRANDEDNESS: SINGLE
TYPE: NUCLEIC ACID
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ORGANISM: Homo sapiens
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Best Local Similarity
                                      LINEAR
E: DNA
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Matches 14; Conserv
                                                        MOLECULE TYPE: 1
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Matches
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US-60-082-614-1535/c
US-60-082-614-1535, Application US/60082614
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
APPLICANT: Blumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a
; TITLE OF INVENTION: high density disequil
; VUMBER OF SEQUENCES: 2730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                               Sequence 20, Application US/10742649
GENERAL INFORMATION:
APPLICANT: Belimfont, Claudia
APPLICANT: Snaid: Jiri
TITLE OF INVENTION: METHOD FOR SPECIFIC FAST DETECTION OF
TITLE OF INVENTION: MELEVANT BACTERIA IN DRINKING WATER
TITLE OF INVENTION: WELEVANT BACTERIA IN DRINKING WATER
FILE REPEBENCE: MANNAH. 10661
CURRENT APPLICATION NUMBER: US/10/742,649
CURRENT APPLICATION NUMBER: DE 10
PRIOR APPLICATION NUMBER: PCT/EP02/06809
PRIOR PLILNG DATE: 2002-06-19
PRIOR PLILNG DATE: 2001-06-19
PRIOR PLILNG DATE: 2001-06-19
PRIOR PRILNG DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.6%; Score 13.4; DB 1; Length 19; Best Local Similarity 93.3%; Pred. No. 6e+02; Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENSET.020PR
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APPLICATION NUMBER: US/60/082,614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Oligonucleotide US-10-742-649-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: GENSE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPHONE: (619) 235-8550
INFORMATION FOR SEQ ID NO: 1535:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Diego
STATE: California
COUNTR: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Win95
SOFTWARE: Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1010 CACCTGAAAAAAGAGG 1024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACCGGAAAAAGAGG 1
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STRET: 5u. ..
CITY: San Diego
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CLASSIFICATION:
                                    -10-742-649-20/C
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 20
LENGTH: 19
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Sequence 142, Application US/10317277A

Sequence 142, Application US/10317277A

Sequence 142, Application US/10317277A

General INFORMATION:

APPLICANT: Dobie, Kenneth W.

TITLE OF INVENTION: Modulation of Estrogen-Responsive Finger Protein Expression

FILE REPERENCE: RTS-0473

CURRENT APPLICATION UNDER: US/10/317,277A

CURRENT PILING DATE: 2002-12-10

NUMBER OF SEQ ID NOS: 168

SOFTWARE: Patentin version 3.2

SEQ ID NO 142

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dobie, Kenneth W.
TITLE OF INVENTION: Modulation of Estrogen-Responsive Finger Protein Expression
FILE REPERBINGS: RTS-0473
CURRENT APPLICATION NUMBER: US/10/317,277A
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 168
SEQ ID NO 67
LENGTH: 20
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) NAME/KEY: upstream amplification primer for SEQ ID229 and SEQ ID882; LOCATION: 1..19
US-60-082-614-1535
                                                                                                                                                              Gaps
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                                                                                                        0.6%; Score 13.4; DB 1; Length 19; 93.3%; Pred. No. 6e+02; tive 0; Mismatches 1; Indels
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| LOCATION: (5016571)...(5016588)
| CTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 554
| PCT-US02-25943-51780
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. OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 646
PCT-US02-25943-60330
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APPLICANT: Saunders, Aleister J. APPLICANT: Mullin, Katina M. APPLICANT: Sampson, Andrew Johnson APPLICANT: Blacker, Deborah Lynne TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US02-25943-60330/c
PCT-US02-25943-60330, Application PC/TUS0225943
; Sequence 60330, Application PC/TUS0225943
; GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas acruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: PTOPICEATY
; SOFTWARE: PTOPICEATY
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                                                                                                                                                                                                                                           Length
                         ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
                                                                                                                                                                                                                                       0.6%; Score 13.2; DB 1;
83.3%; Pred. No. 6.1e+02;
tive 0; Mismatches 3;
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Pred. No. 6.1e+02;
0; Mismatches 3;
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CURRENT APPLICATION NUMBER: PCT/US02/34679
CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: US 60/339,525
PRIOR PELING DATE: 2001-10-25
PRIOR PELING DATE: 2001-11-08
PRIOR PILING DATE: 2001-11-08
PRIOR PILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/336,929
PRIOR APPLICATION NUMBER: US 60/338,363
PRIOR PILING DATE: 2001-11-08
PRIOR PILING DATE: 2001-11-08
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                                                                                                                                                                                                                                                                                                                                                                         1120 CCCAGTTCCACCTTCACC 1137
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APPLICANT: Vellociebi, Gonul
APPLICANT: Blliot, Kathryn J.
APPLICANT: Wang, Xin
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Best Local Similarity 83.3
Matches 15; Conservative
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Matches 15; Conservative
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APPLICANT:
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RESULT 962
FCT-UGGJ-0837-165
Sequence 165, Application PC/TUS0208937
GENERAL INFORMATION:
APPLICANT: THE REGENER OF THE UNIVERSITY OF CALIFORNIA
TITLE OF INVENTION: LEINAMYTICN BIOSYNTHESIS GENE CLUSTER AND ITS COMPONENTS AND THEIR
FILE REPRENCE: 3007-000110PC
CURRENT APPLICATION NUMBER: PCT/US02/08937
CURRENT APPLICATION NUMBER: DCT/US02/08937
CURRENT APPLICATION NUMBER: US 60/278,935
PRIOR APPLICATION WUMBER: US 60/278,935
NUMBER: OF SEQ ID NOS: 222
SOFTWARE: Patentin version 3.0
SET OF THE COMPANY OF THE COMPONENT OF THE COM
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SEGREAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Peeudomonas aeruqinosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PCT/US02/25943
CURRENT FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 64158
SEQ ID NO 51780
LENGTH: 18
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TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REPERENCE: Jim Zegeer Law Offices - 703-684-833
CURRENT APPLICATION NUMBER: PCT/USO2/25943
CURRENT FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 64158
SOFTWARE: Proprietary
SEQ ID NO 29066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Synthetic oligonucleotide PCR primer.
PCT-US02-08937-165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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Best Local Similarity 83.3
Matches 15; Conservative
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Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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PRIOR APPLICATION NUMBER: US 60/337,052

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APPLICANT: Sowert, Lex M.
APPLICANT: Cowsert, Lex M.
APPLICANT: Cowsert, Lex M.
APPLICANT: Baker, Brenda F.
APPLICANT: Sasmor, Henri M.
APPLICANT: Sasmor, Henri M.
APPLICANT: Sasmor, Henri M.
APPLICANT: Sasmor, Henri M.
APPLICANT: Brocks, Douglas G.
APPLICANT: Brocks, Douglas G.
APPLICANT: Myatt, Jacqueline R.
APPLICANT: Myatti Jacqueline R.
TITLE OF INVENTION: Identification of Generation of Oligonucleotides for Generation of Oligonucleotides for Generation Prize REPERENCE: ISIS-3456
CURRENT APPLICATION NUMBER: US 09/067,638
EARLIER PILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
                                                                  GENERAL INFORMATION:

APPLICANT: Reating, Mark T.

APPLICANT: Sanguinetti, Michael C.

APPLICANT: Sanguinetti, Michael C.

APPLICANT: Splawski, Igor

ITILE OF INVENTION: MUTATIONS IN THE KCNEI GENE ENCODING HUMAN mink WHICH

ITILE OF INVENTION: MUTATIONS IN THE KCNEI GENE

TITLE OF INVENTION: KCNEI AS AN LQT GENE

ITILE OF INVENTION: KCNEI AS AN LQT GENE

TITLE OF INVENTION: WHMBER: PCT/US98/17838

CURRENT APPLICATION NUMBER: PCT/US98/17838

CURRENT PILING DATE: 1997-08-29

EARLIER PILING DATE: 1997-08-29

EARLIER PLING DATE: 1995-10-29

EARLIER PLING DATE: 1995-10-29

EARLIER PLING DATE: 1995-12-22

EARLIER PLING DATE: 1995-12-22

EARLIER PLING DATE: 1996-07-29

NUMBER OF SEQ ID NOS: 114

SOFTWARE PARCHING VET: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.6%; Score 13.2; DB 1;
83.3%; Pred. No. 6.1e+02;
live 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 26, Application PC/TUS9908268
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1253 CCATCCCCAACCCCCTTC 1270
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ORGANISM: Artificial Sequence
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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                                             PCT-US98-17838-74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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APPLICANT: Sampson, Andrew Johnson
APPLICANT: Sampson, Andrew Johnson
APPLICANT: Blacker, Deborah Lyune
ITILE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
ITILE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
ITILE OF INVENTION: NEURODEGENERATIVE DISEASES
FILE REFERENCE: 37481-3308pc
CURRENT APPLICATION NUMBER: DCT/US02/34679
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 60/339,525
PRIOR APPLICATION NUMBER: US 60/336,929
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-04
PRIOR APPLICATION NUMBER: US 60/337,052
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US 60/337,052
PRIOR FILING DATE: 2001-13-04
PRIOR FILING DATE: 2001-10-05
PRIO
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Pred. No. 6.1e+02;
0; Mismatches 3; Indels
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PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US 60/368,919
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 564
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 343, Application PC/TUS0234679
GENERAL INFORMATION:
APPLICANT: Becker, Kenneth David
APPLICANT: Velicelebi, Gonul
APPLICANT: Bliot, Kathryn J.
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Tanzi, Rudolph E.
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Saunders, Aleister J.
Mullin, Kristina M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dáaddcadarcaaccir 18
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Best Local Similarity 83.3v
-hes 15; Conservative
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                         TYPE: DNA
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Pred. No. 6.1e+02;
0; Mismatches 3; Indels
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APPLICANT: Sanguinetti, Michael C.
APPLICANT: Curran, Mark E.
APPLICANT: Curran, Mark E.
APPLICANT: Curran, Mark E.
APPLICANT: Landes, Gregory M.
APPLICANT: Landes, Gregory M.
APPLICANT: Burn, Timothy D.
APPLICANT: Burn, Timothy C.
APPLICANT: Splawski, Igor
TITLE OF INVENTION: KYLOT1 - A LONG OT SYNDROME GENE FILE REFERENCE: 2323-133
CURRENY FILING DATE: 1999-06-12
EARLIER APPLICATION NUMBER: 60/094,477
EARLIER APPLICATION NUMBER: 08/921,068
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 08/739,383
EARLIER FILING DATE: 1996-10-29
EARLIER FILING DATE: 1995-12-22
MUMBER FILING DATE: 1995-12-22
MUMBER FILING DATE: 1995-12-22
MUMBER FILING DATE: 1995-12-22
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                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/071,433
FILING DATE: March 12, 1999
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERRNCE/DOCKET NUMBER: ISPH-0355
         APPLICATION NUMBER: PCT/US99/08765A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-CS99-10260-74; Sequence 74, Application PC/TUS9910260; GENERAL INFORMATION:
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                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 810-1515
TELEPAX: (609) 810-1454
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 TAGACACCTGGAACAGAG 1
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Best Local Similarity 83.3%;
Matches 15; Conservative (
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                                 Herewith
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STRANDEDNESS: singl
TOPOLOGY: linear
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                               FILING DATE: H
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PCT-US99-08765A-26
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US-08-489-967-1
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LENGTH: 18
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APPLICANT: Borchers, Alexander.
APPLICANT: Borchers, Timothy A.
TITLE OF INVENTION: Identification of Genetic Targets for Modulation by
TITLE OF INVENTION: Oligonucleotides and Generation of Oligonucleotides for Gene
FILE REFRENCE: ISS.3456
CURRENT APPLICATION NUMBER: PCT/US99/08268
CURRENT FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: US 09/067,638
EARLIER FILING DATE: 1998-04-28
EARLIER FILING DATE: 1998-04-28
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
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0.6%; Score 13.2; DB 1; Length 18; 83.3%; Pred. No. 6.1e+02; Live 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: C. Frank Bennett and Lex M. Cowsert TITLE OF INVENTION: ANTISENSE MODULATION OF TITLE OF INVENTION: CD40 EXPRESSION NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata STREET: 66 E. Main Street
CITY: MarIton
Smare ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Antisense Oligonucleotide PCT-US99-08268-221
                                                                                                                                                                                                                              PCT-US99-08268-221/C
; Sequence 221, Application PC/TUS9908268
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
; APPLICANT: Gowsert, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: Breier, Susan M.
; APPLICANT: Sasmor, Henri M.
; APPLICANT: Sasmor, Henri M.
; APPLICANT: Object, Douglas G.
; APPLICANT: Object, Jacqueline R.
; APPLICANT: Object, Jacqueline R.
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COMPUTER: 1BM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect 6.0
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; Sequence 26, Application PC/TUS9908765A
SEQUENCE 26, Application PC/TUS9908765A
SEQUENCE 26, Application PC/TUS9908765A
SEQUENCE 26, Application PC/TUS9908765A
                                                                                           1006 TCGACACCTGAAAAGAG 1023
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                                                                                                                                         18 TAGACACCTGGAACAGAG
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                          Best_Local Similarity 83.3
Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserv
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ZIP: 08053
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LENGTH: 18
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    Query Match
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Gaps
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APPLICANT: Timothy A. Vickers
TITLE OF INVENTION: Identification of Genetic
TITLE OF INVENTION: Targets for Modulation By Oligonucleotides and
TITLE OF INVENTION: Generation of Oligonucleotides for Gene
TITLE OF INVENTION: Modulation
MUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOOLOCK WASHBURN KURTZ
ADDRESSEE: MODCOCK WASHBURN KURTZ
STREET: 1 LIBERTY PLACE 46TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM
OPERATING SYSTEM: PC-Windows NT
SOCHWARE: WORD PERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,638B
FILING DATE: 28-APR-1998
CLASSIFICATION NUMBER: 60/081,483
RICHATION NUMBER: 60/081,483
APPLICATION NUMBER: 60/081,483
ATTORNEY/AGENT INFORMATION:
NAME: JOHN W. CALDAMALI
RESISTRATION NUMBER: 28,937
REFERENCE/DOCKET NUMBER: 1SIS-2960
                            NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE, POCKET NUMBER: ATGS0032
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5119
TELEFRAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/09067638B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lex M. Cowsert
Brenda F. Baker
John McNeil
Susan M. Freier
Henri M. Sasmor
Douglas G. Brooks
Cara Ohashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       853 GAGAATGTTAAGGGCACT 870
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         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                            linear
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MOLECULE TYPE: ci
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-969-330-47
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US-09-067-638B-26/c
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APPLICANT:
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                   APPLICANT: Studier, F. W.
APPLICANT: Dunn, John J.
TITLE OF INVENTION: SYNTHESIS OF DNA BY HEXAMER LIGATION
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brookhaven National Laboratory
STREET: Building 902C
CITY: Upton
STATE: New York
COUNTRY: US
                                                                                                                                                                                                                                                ZIP: 11973

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/489,967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SmithKline Beecham Corporation
APPLICANT: Thomas Jefferson University
TITLE OF INVENTION: HRAD54
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,676
FILING DATE: November 13, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-969-330-47/c; Sequence 47, Application US/08969330; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAT, MATGARET
REGISTRATION NUMBER: 25,324
REFRENCE/DOCKET NUMBER: AUI
TELECOMMUNICATION INFORMATION:
TELEFONE (516) 282-7338
TELEFAX: (516) 282-7338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            965 AACGGTGGAAGTCCAAGC 982
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                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-489-967-1
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JAPPLICANT: Cowsert, Lex M.

APPLICANT: Baker, Brenda F.

APPLICANT: Baker, Brenda F.

APPLICANT: Baker, Susan M.

APPLICANT: McNeil, John

APPLICANT: Brooks, Douglas G.

APPLICANT: Brooks, Douglas G.

APPLICANT: Brooks, Douglas G.

APPLICANT: Brooks, Douglas G.

APPLICANT: Watt, Jacqueline R.

APPLICANT: Worthers, Alexander

APPLICANT: Worthers, Alexander

APPLICANT: Worthers, Timothy A.

ITTLE OF INVENTION: Identification of Genetic Targets for Modulation by

ITTLE OF INVENTION: Oligonucleotides and Generation of Oligonucleotides for Gene

TITLE OF INVENTION: WOMBER: US/09/295,463

ITTLE OF INVENTION: Modulation

FILE REFERENCE: ISIS-3455

CURRENT APPLICATION NUMBER: US/09/295,463

CURRENT PILING DATE: 1999-04-13

EARLIER FILING DATE: 1998-04-13

EARLIER FILING DATE: 1998-04-13

EARLIER PILING DATE: 1998-04-13

EARLIER PILING DATE: 1998-04-13

ERRIER OF SEQ ID NOS: 372

LENGTH: 18
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                                                                                                                                                                                                                                                                                                                           Query Match
0.6%; Score 13.2; DB 1;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3;
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0.6%; Score 13.2; DB 1;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Antisense Oligonucleotide US-09-295-463-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Antisense Oligonucleotide
                                                    60/081,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 1083, Application US/09541946; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-295-463-221/c
; Sequence 221, Application US/09295463
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            1006 TCGACACCTGAAAAAGAG 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1120 CCCAGTTCCACCTTCACC 1137
                  EARLIER FILING DATE: 1998-04-28
EARLIER APPLICATION NUMBER: US 6
EARLIER FILING DATE: 1998-04-13
NUMBER OF SEQ ID NOS: 372
SEQ ID NO 26
LENGTH: 18
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APPLICANT: Cargill, Michele
APPLICANT: Altshuler, David M.
APPLICANT: Ireland, James S.
APPLICANT: Sklar, Pamela
APPLICANT: Patil, Nila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 radacaccregaacagag 1
                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
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US-09-541-946-1083
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GENURRAL INFORMATION:
APPLICANT: Coweart, Lex M.
APPLICANT: Baker, Brenda F.
APPLICANT: Baker, Brenda F.
APPLICANT: Rouell, John
APPLICANT: Sasun M.
APPLICANT: Sasun M.
APPLICANT: Sasun M.
APPLICANT: Sasun M.
APPLICANT: Wath, Cara M.
APPLICANT: Wath, Jacqueline R.
APPLICANT: Wath: Jacqueline R.
APPLICANT: Wath: Alexander
APPLICANT: Wath: Alexander
APPLICANT: Wath: Management of Genetic Targets for Modulation by
TITLE OF INVENTION: Oligonucleotides and Generation of Oligonucleotides for Gene
FILE REFERENCE: ISIS-3455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 72, Application US/09135021

GENERAL INFORMATION:
APPLICANT: Splawski, Igo
PAPLICANT: Splawski, Igo
TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQTI WHICH CAUSES JERVELL
TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
ITLE REFERENCE: 2323-128
CURRENT APPLICATION NUMBER: US/09/135,021
EARLIER APPLICATION NUMBER: 08/09/135,021
EARLIER APPLICATION NUMBER: 08/09/135
EARLIER FILING DATE: 1998-08-17
EARLIER FILING DATE: 1998-07-06-13
EARLIER FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 13.2; DB 1; Length 18;
Pred. No. 6.1e+02;
0; Mismatches 3; Indels
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CURRENT FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: US 09/067,638
                                                                                                                                                                                                                                                                                                                                                                                  1006 TCGACACCTGAAAAAGAG 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1253 CCATCCCCAACCCCCTTC 1270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    18 TAGACACCTGGAACAGAG 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-135-021-72
                                                                                                                                                                                                     ;
TOPOLOGY:
US-09-067-638B-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 977
US-09-295-463-26/c
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US-09-135-021-72
                                                                                                                              LENGTH:
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APPLICANT: VIDER
TITLE OF INVENTION: METHOD OR IDENTIFYING AND CHARACTERIZING CELLS AND TISSUES
FILE REFERENCE: 24296
FURRENT APPLICATION NUMBER: US/09/582,533A
CURRENT FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 286
SEQ ID NO 251
LENGTH: 18
                               APPLICANT: Stlat, Pamela
APPLICANT: Stlat, Pamela
APPLICANT: Datil, Nila
APPLICANT: Lipshutz, Poert J.
APPLICANT: Lipshutz, Poert J.
APPLICANT: Lipshutz, George Q.
TITLE OF INVENTION: CHARACTERIZATION OF SINGLE NUCLEOTIDE
TITLE OF INVENTION: POLYMORPHISMS IN CODING REGIONS OF HUMAN GENES
TILE REPERENCE: 2825.1017-003
CURRENT APPLICATION NUMBER: US/09/541,946
CURRENT APPLICATION NUMBER: US/09/541,946
PRIOR PRILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 2889
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 18
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GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF ELK-1 EXPRESSION
FILLE REPRENCE: RYSP-0127
CURRENT APPLICATION NUMBER: US/09/868,301
CURRENT PILING DATE: 2001-06-15
NUMBER OF SEQ ID NOS: 47
: LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 13.2; DB 1;
Pred. No. 6.1e+02;
0; Mismatches 3;
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Pred. No. 6.1e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: Oligonucleotide primer US-09-541-946-1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-582-533A-251; Sequence 251, Application US/09582533A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1197 GGCACCACCCTATCAGGG 1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1093 ACCCCCACCCTGGGCTTC 1110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.6%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
                        Ireland, James S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 83.33
Matches 15; Conservative
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APPLICANT: Cargill, Michele
APPLICANT: Altshuler, David M.
APPLICANT: Altshuler, David M.
APPLICANT: Altshuler, David M.
APPLICANT: Internated, James S.
APPLICANT: Batil, Nila
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Daley, George Q.
TITLE OF INVENTION: CHARACTERIZATION OF SINGLE NUCLEOTIDE
TITLE OF INVENTION: CHARACTERIZATION OF SINGLE NUCLEOTIDE
TITLE OF INVENTION: CHARACTERIZATION OF HUMAN GENES
TITLE OF INVENTION: CHARACTERIZATION OF HUMAN GENES
TITLE OF TALING DATE: 1099-03-31
PRIOR APPLICATION NUMBER: US 60/127,248
PRIOR PILING DATE: 1099-03-31
NUMBER OF SEQ ID NOS: 2889
SEQ ID NO 1090
SEQ ID NO 1090
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
APPLICANT: Lipshutz, Robert J.
APPLICANT: Daley, George Q.
TITLE OF INVENTION: CHARACTERIZATION OF SINGLE NUCLEOTIDE
TITLE OF INVENTION: CHARACTERIZATION OF SINGLE NUCLEOTIDE
TITLE OF INVENTION: POLYMORPHISMS IN CODING REGIONS OF HUMAN GENES
FILE REFERENCE: 2225.1017-003
CURRENT APPLICATION NUMBER: US 60/127,248
PRIOR APPLICATION NUMBER: US 60/127,248
NUMBER OF SEQ ID NOS: 2889
SOFTWARE: FRALES FARLES for Windows Version 4.0
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Pred. No. 6.1e+02;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: Oligonucleotide primer US-09-541-946-1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Oligonucleotide primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1090, Application US/09541946 GENERAL INFORMATION:
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; GENERAL INFORMATION:
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APPLICANT: Cargill, Michele
APPLICANT: Altshuler, David M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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Best Local Similarity 83.33
Matches 15, Conservative
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Best Local Similarity 83.3
Matches 15, Conservative
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US-09-541-946-1101
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LENGTH: 18
                                                                                                                                                                                                                                                                                                               TYPE: DNA
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Sequence 74, Application US/10138316

GENERAL INFORMATION:

APPLICANT: Keating, Mark T.

APPLICANT: Sanguinetti, Michael C.

APPLICANT: Sanguinetti, Michael C.

APPLICANT: Sanguinetti, Michael C.

APPLICANT: Sanguinetti, Michael C.

TITLE OF INVENTION: MTATIONS IN THE KCNEI GENE ENCODING HUMAN minK WHICH

TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING

TITLE OF INVENTION: MYBBER: US/10/138,316

FILE REFERENCE: 2323-162

CURRENT APPLICATION NUMBER: 09/44,295

PRIOR APPLICATION NUMBER: 09/44,295

PRIOR APPLICATION NUMBER: 09/135,020

PRIOR APPLICATION NUMBER: 08/921,068

PRIOR PILING DATE: 1999-10-29

PRIOR PILING DATE: 1996-10-29

PRIOR PILING DATE: 1996-10-29

PRIOR APPLICATION NUMBER: 60/019,014

PRIOR APPLICATION NUMBER: 60/019,014

PRIOR APPLICATION NUMBER: 60/094,477

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Sequence 29066, Application US/10227565
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Peeudomonas aeruginosa PAO1, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SOFTWARE: Proprietary
SEQ ID NO 29066
LINGTH: 18
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                        Length 18;
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                      Score 13.2; DB 1;
Pred. No. 6.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 13.2; DB 1; 83.3%; Pred. No. 6.1e+02;
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83.3%; Pred. No. 6.1e+02;
              Query Match 0.6%; Score 13.2; D
Best Local Similarity 83.3%; Pred. No. 6.1e
Matches 15; Conservative 0; Mismatches
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                                                                                                           1006 TCGACACCTGAAAAGAG 1023
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Best Local Similarity 83.3
Matches 15; Conservative
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Best Local Similarity
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APPLICANT: Borchers, Alexander
APPLICANT: Borchers, Timothy A.
TITLE OF INVENTION: Identification of Genetic Targets For Modulation By Oligonucleotif
TITLE OF INVENTION: Generation of Oligonucleotides For Gene Modulation
FILE REFERENCE: ISISSO26
CURRENT APPLICATION WUMBER: 104-04-04
PRIOR APPLICATION WUMBER: 09/067,638
PRIOR APPLICATION NUMBER: 09/067,638
PRIOR APPLICATION NUMBER: 00/081,483
PRIOR APPLICATION NUMBER: 60/081,483
PRIOR FILING DATE: 1998-04-13
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn version 3.1
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                                                                               Length 18;
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APPLICANT: Brenda F. Baker
TITLE OF INVENTION: ANTISENSE MODULATION OF ELK-1 EXPRESSION
FILE REPERENCE: RISP-0127
CURRENT APPLICATION NUMBER: US/09/868,301A
CURRENT FILING DATE: 2001-06-15
NUMBER OF SEQ ID NOS: 47
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                                                                                                                          Indels
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Pred. No. 6.1e+02;
0; Mismatches 3; Indels
                                                                     Score 13.2; DB 1;
Pred. No. 6.1e+02;
                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                           US-09-868-301A-24/c; Sequence 24, Application US/09868301A; GENERAL INFORMATION:
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APPLICANT: Cowsert, Lex M.
APPLICANT: Baker, Brenda F.
                                                                                                                                                               1120 CCCAGTTCCACCTTCACC 1137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McNeil, John
Freier, Susan M.
Sasmor, Henri M.
Brocks, Douglas G.
Ohashi, Cara
Wyatt, Jacqueline R.
                                                                                                                                                                                                            18 crcrarrccaccrrcacc 1
                                                                Query Match 0.6%;
Best Local Similarity 83.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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OTHER INFORMATION: Synthetic
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Best Local Similarity 83.3
Matches 15; Conservative
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  ; OTHER INFURE
US-09-868-301-24
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LENGIH: 18
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LENGTH: 18
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Sequence 40503. Application US/10266090
GENERAL INFORMATION:
APPLICANT: GOFF, STEPHEN
APPLICANT: GOFF, STEPHEN
APPLICANT: GOLBERT, MICHELLE
APPLICANT: COLBERT, MICHELLE
APPLICANT: WANG, WENG-LIN
ITILE OF INVENTION: CRERAL TRINUCLEOTIDE SIMPLE SEQUENCE
ITILE OF INVENTION: REPEAT MARKERS AND THEIR USES
FILE REPERENCE: MADII. 05801
CURRENT APPLICATION NUMBER: US/10/266,090
CURRENT FILING DATE: 2002-10.03
PRIOR FILING DATE: 2002-09-26
PRIOR PLICATION NUMBER: US 60/326,117
PRIOR PLICATION NUMBER: US 60/326,117
PRIOR PLICATION NUMBER: 2001-09-26
NUMBER OF SEQ ID NOS: 51812
SEQ ID NO 40503
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA US-10-266-090-38112
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 18;
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    ; TITLE OF INVENTION: CEREAL TRINUCLECTIDE SIMPLE SEQUENCE; TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES.
; FILE REPERENCE: NADII. 058C1; CURRENT APPLICATION NUMBER: US/10/266,090; CURRENT FILING DATE: 2002-10-03; PRIOR APPLICATION NUMBER: US 10/260,703; PRIOR PILING DATE: 2002-09-26; PRIOR APPLICATION NUMBER: US 60/326,117; PRIOR FILING DATE: 2001-09-26; PRIOR FILING DATE: 2001-09-26; NUMBER OF SEQ ID NOS: 51812; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 38112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
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APPLICANT: GOFF, STEPHEN
APPLICANT: BONAN, CAROLINE
APPLICANT: WANG, RONG-LIN
APPLICANT: WANG, RONG-LIN
TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.6%; Score 13.2; DB 1; Best Local Similarity 83.3%; Pred. No. 6.1e+02; Matches 15; Conservative 0; Mismatches 3;
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83.3%; Pred. No. 6.1e+02;
tive 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.3
Matches 15; Conservative
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CHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 55445
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CIHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 64604
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                                                                                                                                       RESULT 988
US-10-227-565-51780
Sequence 51780
Sequence 51780
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE PEPERENT APPLICATION: DATE: 2002-08-26
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SOFTWARE: Proprietary
SEQ ID NO 51780
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PAO1, complete genome.
FILE REPERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: U$/10/227,565
CURRENT FILING DATE: 2002-08-26
SOFTWARE: Proprietary
SEQ ID NOS: 64158
SOFTWARE: Proprietary
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83.3%; Pred. No. 6.1e+02;
ative 0; Mismatches 3; Indels
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ive 0; Mismatches 3; Indels
       Indels
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    Mismatches
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; Sequence 38112, Application US/10266090
; GENERAL INFORMATION:
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                                             1119 GCCCAGTTCCACCTTCAC 1136
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                                                                                       18 GGCCAGTTCGTCCTTCAC 1
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APPLICANT: BONAN, CAROLINE
APPLICANT: COLBERT, MICHELLE
APPLICANT: WANN, RONG-LIN
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Best Local Similarity 83.33
Matches 15; Conservative
    Conservative
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Best Local Similarity
Matches 15; Conserv
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APPLICANT: Bertram, Larg
APPLICANT: Saunders, Aleister J.
APPLICANT: Saunders, Aleister J.
APPLICANT: Saunders, Aleister J.
APPLICANT: Mullin, Kristina M.
APPLICANT: Mullin, Kristina M.
APPLICANT: Blacker, Deborah Lynne
APPLICANT: Blacker, Deborah Lynne
APPLICANT: Blacker, Deborah Lynne
TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROWOSOME 10
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISBASE AND OTHER
TITLE OF INVENTION: NEURODEGENERATIVE DISBASES
TITLE REFRENCE: 37481-3308
CURRENT APPLICATION NUMBER: US 60/339,525
PRIOR APPLICATION NUMBER: US 60/339,010
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
PRIOR PELING DATE: 2001-11-09
PRIOR PELING DATE: 2001-11-09
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-13-08
NUMBER OF SEQ ID NOS: 564
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 341
                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA US-10-266-090-51728
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13.2; DB 1; Length 18; Pred. No. 6.1e+02; 0; Mismatches 3; Indels
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                                       CURRENT APPLICATION NUMBER: US/10/266,090
CURRENT FILING DATE: 2002-10-03
FRIOR APPLICATION NUMBER: US 10/260,703
FRIOR FILING DATE: 2002-09-26
FRIOR APPLICATION NUMBER: US 60/326,117
FRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 51812
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51728
LENGTH: 18
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GENERAL INFORMATION:
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Elliot, Kathryn J
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Best Local Similarity 83.33
Matches 15; Conservative
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Best Local Similarity
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CHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-47008
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APPLICANT: GOFF, STEPHEN
APPLICANT: GOFF, STEPHEN
APPLICANT: COLEMET, MICHELLE
APPLICANT: COLEMET, MICHELLE
APPLICANT: WANG, RONG-LIN
TITLE OF INVENTION: CEREAL TRINUCLECTIDE SIMPLE SEQUENCE
TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
FILE REFERENCE: NADII.058C1
CURRENT APPLICATION NUMBER: US/10/266,090
CURRENT APPLICATION NUMBER: US 10/260,703
PRIOR APPLICATION NUMBER: US 60/326,117
PRIOR PILING DATE: 2002-09-26
NUMBER OF SEQ ID NOS: 51812
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51552
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Sequence 51728.
Sequence 51728.
Sequence 51728.
Sequence 51728.
September 3 Application US/10266090
GENERAL INFORMATION:
APPLICANT: GOLBERT, MICHELLE
APPLICANT: COLBERT, MICHELLE
APPLICANT: WANG, RONG-LIN
TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
FILE REFERENCE: NADII.058C1
CURRENT APPLICATION NUMBER: US/10/266,090
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: US 60/326,117
PRIOR PILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/326,117
PRIOR PILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 51812
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 47008
LENGTH: 18
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.3%;
Matches 15; Conservative
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ORGANISM: Artificial Sequence
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Matches 15; Conservative
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US-10-266-090-51552
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US-10-293-338-6601
Sequence 6601, Application US/10293338
GENERAL INFORMATION:
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TITLE OF INVENTION:
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TITLE 
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GENERAL INFORMATION:
APPLICANT: ROSELtaGenemics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
CURRENT APPLICATION UNMBER: US/10/303,778
CURRENT PILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 17608
SOFTWARE: Patentin version 3.1
SEQ ID NO 3233
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 47416
CURRENT APPLICATION REGULATORY GENES AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/303,778
CURRENT FILING DATE: 2002-11-26
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    Score 13.2; DB 1;
Pred. No. 6.1e+02;
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Pred. No. 6.1e+02;
0; Mismatches 3;
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Query Match 0.6%;
Best Local Similarity 83.3%;
Matches 15; Conservative
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Best Local Similarity 83.37
Thes 15; Conservative
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; ORGANISM: Homo sapiens
US-10-293-338-6601
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; ORGANISM: Homo sapiens
US-10-303-778-3233
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US-10-303-778-4618/c
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Sequence 2066, Application US/10293338
Sequence 2066, Application US/10293338
Sequence 2066, Application
Sequence 2066
Sequ
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APFLICANT: Blacker, Deborah Lynne
TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
TITLE OF INVENTION: MENGADEGENERATIVE DISEASES
FILE REFERENCE: 37481-3308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           o;
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Pred. No. 6.1e+02;
0; Mismatches 3; Indels
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CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: US 60/339,525
PRIOR FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 60/338,010
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
PRIOR PLING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/336,363
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-12-04
PRIOR PRIOR APPLICATION NUMBER: US 60/368,919
PRIOR FILING DATE: 2001-12-04
PRIOR PLING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 564
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 343
                                                                                                                                                                                                                                             Sequence 343, Application US/10282174 GENERAL INFORMATION:
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Saunders, Aleister J.
Mullin, Kristina M.
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APPLICANT: Velicelebi, Gonul
APPLICANT: Elliot, Kathryn J.
                       1 CGAGCCCAGATCAACCTT 18
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Best Local Similarity 83.3%;
Matches 15; Conservative
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; ORGANISM: Homo sapiens
US-10-293-338-2066
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APPLICANT:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROSectadenomics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
TITLE OF INVENTION: REGILATORY GENES AND USES THEREOF
FILE REPERENCE: 47416
CURRENT APPLICATION UNMERR: US/10/303,778
CURRENT APPLICATION UNMERR: 105/10/303,778
NUMBER OF SEQ ID NOS: 17608
SOFTWARE: Patentin version 3.1
SEQ ID NO 4666
LENGTH: 18
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROSectaGenomics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
FILE REFERENCE: 47416
CURRENT APPLICATION UNDER: US/10/303,778
CURRENT FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 17608
SOFTWARE: PATENTIN Version 3.1
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83.3%; Pred. No. 6.1e+02;
tive 0; Mismatches 3; Indels
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Pred. No. 6.1e+02;
0; Mismatches 3;
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NUMBER OF SEQ ID NOS: 17608
SOFTWARE: Patentin version 3.1
SEQ ID NO 4618
LENGTH: 18
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Best Local Similarity 83.33
Matches 15; Conservative
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Best Local Similarity 83.3
Matches 15; Conservative
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                                                                           TYPE: DNA
ORGANISM: Homo sapiens
US-10-303-778-4618
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CORGANISM: Homo sapiens
US-10-303-778-4999
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ORGANISM: Homo sapiens
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US-10-303-778-4999/c
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RESULT 1003 US-10-303-778-8192/c

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US-10-310-188-4288/c

US-10-310-188-4288/c

Sequence 4288, Application US/10310188

Sequence 4288, Application US/10310188

Sequence 4288, Application US/20310188

TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GET

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

CURRENT APPLICATION NUMBER: US/10/310,188

CURRENT FILING DATE: 2002-12-19

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: Patentin version 3.1

SEQ ID NO 4288

LENGTH: 18
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Sequence 5478, Application US/10310188

Sequence 5478, Application US/10310188

GENERAL INFORMATION:

APPLICANT: ROSettaGemonics

TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

CURRENT APPLICATION NUMBER: US/10/310,188

CURRENT FILING DATE: 2002-12-19

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: Patentin version 3.1

SEQ ID NO 5478

LENGTH: 18
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                                           APPLICANT: Rosettagenomics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
FILE REPREBNCE: 47416
CURRENT APPLICATION NUMBER: US/10/303,778
CURRENT FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 17608
SOFTWARE: Patentin version 3.1
LENGTH: 18
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Pred. No. 6.1e+02;
0; Mismatches 3; Indels
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0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels
Sequence 8192, Application US/10303778 GENERAL INFORMATION:
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Best Local Similarity 83.33
Matches 15, Conservative
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Best Local Similarity 83.33
Matches 15; Conservative
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CORGANISM: Homo sapiens
US-10-310-188-4288
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US-10-303-778-8192
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US-10-310-188-5478
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LENGTH: 18

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Sequence 11033, Application US/10310188
GENERAL INFORMATION:
APPLICANT: ROSELEGEmonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GE
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER: OF SEQ ID NOS: 86841
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 11033
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ve 0; Mismatches 3; Indels
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33.3%; Pred. No. 6.1e+02;
ive 0; Mismatches 3;
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US-10-110-188-17069
Sequence 17069, Application US/10310188
GENERAL INFORMATION:
APPLICANT: RosettaGemonics
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Best Local Similarity 83.34
Matches 15; Conservative
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      TYPE: DNA
GRGANISM: Homo sapiens
US-10-310-188-9706
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Matches 15; Conserv
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Matches 15; Conserv
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 202-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Parentin version 3.1
LENGTH: 18
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US-10-188-9659/C

US-10-188-9659/C

GENERAL INFORMATION:

APPLICANT: ROSELtaGemonics

TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: 47487

CURRENT APPLICATION UNDER: US/10/310,188

CURRENT APPLICATION UNDER: 202-12-19

NUMBER OF SEQ ID NOS: 86841

SOFTWARE: PATENTING DATE: 202-12-13

SOFTWARE: PATENTING DATE: 205-12-13

SOFTWARE: PATENTING DATE: 205-12-13

LENGTH: 18
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Sequence 9706, Application US/10310188

Sequence 9706, Application US/10310188

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
TITLE
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0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels
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0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.10+02;
Matches 15; Conservative 0; Mismatches 3; Indels
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US-10-310-188-6210
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RESULT 1014
US-10-188-42218/C
US-10-188-42218/C
SEQUENCE ADDITION:
SEQUENCE ADDITION:
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENTINE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: UNBER: US/10/310,188
CURRENT APPLICATION UNBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SEQ ID NO 42218
LENGTH: 18
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Sequence 51868, Application US/10310188

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENTILE OF INVENTION: USES THEREOF;

TITLE OF 100 SIR 08

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LENGTH: 18
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US-10-310-1488-58107/c
Sequence 58107, Application US/10310188
Sequence 58107, Application US/10310188
GENERAL INFORMATION:
APPLICANT: ROBERTAGEmonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GETTITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
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Pred. No. 6.1e+02;
0; Mismatches 3; Indels
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33.3%; Pred. No. 6.1e+02;
ive 0; Mismatches 3;
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                    18 CCGGCCCCATCCCCGCCC 1
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Best Local Similarity 83.3%;
Matches 15; Conservative
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Best Local Similarity 83.33
Matches 15, Conservative
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US-10-310-188-51868
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE TITLE OF INVENTION: USES THEREOF FILE REFERENCE: 47487 CURRENT APPLICATION NUMBER: US/10/310,188 CURRENT FILING DATE: 2002-12-19 NUMBER OF SEQ ID NOS: 86841 SOFTWARE PARELE: PARENTIN VERSION 3.1 SEQ ID NO 17069 LENGTH: 18
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 26440
LENGTH: 18
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rosettademonics
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
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Pred. No. 6.1e+02;
0; Mismatches 3; Indels
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Best Local Similarity 83.3%;
Matches 15; Conservative
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Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-17069
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; ORGANISM: Homo sapiens
US-10-310-188-26440
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ORGANISM: Homo sapiens
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US-10-310-188-26440
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LENGTH: 18
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US-10-310-188-72865/c
Sequence 72865, Application US/10310188
Sequence 72865, Application US/10310188
Sequence 72865, Application US/10310188
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GE TITLE REFERENCE: 47487
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER: OF SEQ ID NOS: 86841
SEQ ID NO 72865
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                                                                                                                                                                                               0.6%; Score 13.2; DB 1;
83.3%; Pred. No. 6.1e+02;
tive 0; Mismatches 3;
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Pred. No. 6.1e+02;
0; Mismatches 3;
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Pred. No. 6.1e+02;
0; Mismatches 3;
       CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 69028
LENGTH: 18
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Matches 15; Conservative
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                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-310-188-72865
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Matches 15; Conserv
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Best Local Similarity
Matches 15; Conserv
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PATENTIN VERSION 3.1
LENGTH: 18
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TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THERROF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT APPLICATION NUMBER: 2002-12-19
NUMBER OF SEQ ID NOS: 66841
SOFTWARE: Patentin version 3.1
LENGTH: 18
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US-10-188-69028/C
US-10-188-69028/ Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGemonics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; TITLE OF INVENTION: USES THEREOF
; FILE REFRENCE: 47487
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                                 Query Match 0.6%; Score 13.2; DB 1; Length 18; Best Local Similarity 83.3%; Pred. No. 6.1e+02; Matches 15; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.6%; Score 13.2; DB 1; Length 18; Best Local Similarity 83.3%; Pred. No. 6.1e+02; Matches 15; Conservative 0; Mismatches 3; Indels
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VS-10-310-188-64553
Sequence 64553, Application US/10310188
GENERAL INFORMATION:
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2-10-310-188-64750
; Sequence 64750, Application US/10310188
; GENERAL INFORMATION:
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US-10-310-188-64553
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Best Local Similarity
Matches 15; Conserv
US-10-310-188-58107
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Sequence 85920, Application US/10310188
Sequence 85920, Application US/10310188
GENERAL INFORMATION:
APPLICANT: RosettaGemonics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENTILE OF INVENTION: USES THEREOF
FILE REPERENCE: 47487
CURRENT APPLICATION WINBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: Patentin version 3.1
SEQ ID NO 85920
LENGTH: 18
                                                                                                                                                                                                                   Sequence 85848, Application US/10310188
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE REFRENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
UNUMBER OF SEQ ID NOS: 86841
SEQ ID NO 85848
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Sequence 86807, Application US/10310188

GENERAL INFORMATION:
APPLICANT: ROBELTAGEMONICS
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
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                                     Indels
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           Best Local Similarity 83.3%; Pred. No. 6.1e+02; Matches 15; Conservative 0; Mismatches 3;
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83.3%; Pred. No. 6.1e+02;
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Best Local Similarity 83.37
Thes 15; Conservative
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; ORGANISM: Homo sapiens
US-10-310-188-85848
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Best Local Similarity
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US-10-310-188-85920/c
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US-10-310-188-85848
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; ORGANISM: Homo &
US-10-310-188-85920
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                                     Sequence 75117, Application US/10310188
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BECOME STREET GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
CURRENT APPLICATION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
CURRENT APPLICATION: USES THEREOF
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SEQ ID NO 75117
IENGTH: 18
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SEQ ID NO SEQ ID NOS: 86841
SEQ ID NO 77971
LENGTH: 18
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GENERAL INFORMATION:
APPLICANT: ResettaGemonics
TITLE OF INVENTION: BIOLINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PACHOLIN VERSION 3.1
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Best Local Similarity 83.3
Matches 15; Conservative
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Best Local Similarity 83.3
Matches 15; Conservative
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US-10-310-188-77971
                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
US-10-310-188-75117
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ORGANISM: Homo sapiens
RESULT 1022
US-10-310-188-75117/c
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APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
TITLE OF INVERTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/10/349,143
CURRENT APPLICATION NUMBER: US/09/422,978
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
PRIOR FILING DATE: BARLIER FILING DATE: 1999-04-21
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
NUMBER: OF SEQ ID NOS: 11796
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                            NAME/KEY: primer_bind

: IOCATION: 11.18

: OTHER INFORMATION: upstream amplification primer 99-13332 for SEQ 176,

US-10-349-143-4110
                                                                                                                                                                                                          Gaps
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; Sequence 29066, Application US/10367832A
; GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SEQ ID NO 29066
; LENGTH: 18
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                                                                                                                                                                                                        Indels
                                                                                                                                                           Length
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
                                                                                                                                                      0.6%; Score 13.2; DB 1;
ilarity 83.3%; Pred. No. 6.1e+02;
Conservative 0; Mismatches 3;
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ORGANISM: Homo Sapiens
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                                                                                                                                                      Query Match
Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
Matches 15; Conserv
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APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelle markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/10/349,143
CURRENT ELING DATE: 2003-01-21
PRIOR PELING DATE: 1999-10-20
PRIOR PELING DATE: 1999-10-20
PRIOR PELING DATE: BARLIER APPLICATION NUMBER: US 09/298,850
PRIOR PELING DATE: BARLIER APPLICATION NUMBER: US 60/109,732
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US 60/109,732
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US 60/082,614
PRIOR PILING DATE: BARLIER FILING DATE: 1998-11-23
PRIOR PILING DATE: BARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NOS: 11796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SHEN, Ben
APPLICANT: CHENG, Y1-Qiang
APPLICANT: CHENG, Y1-Qiang
APPLICANT: TREE SHENG, SUIG-
TITLE OF INVENTION: Synthases and Methods of Use
CURRENT APPLICATION NUMBER: US/10/314,657
CURRENT APPLICATION NUMBER: PGT/USO2-12-09
PRIOR APPLICATION NUMBER: PGT/USO2/08937
PRIOR APPLICATION NUMBER: US 60/278,935
PRIOR FILING DATE: 2001-03-26
NUMBER: OF SEQ ID NOS: 214
SOPTWARE: Patentin version 3.2
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Pred. No. 6.1e+02;
0; Mismatches 3; Indels
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Pred. No. 6.1e+02;
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GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
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Best Local Similarity 83.3%;
Matches 15; Conservative
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Best Local Similarity 83.3%;
Matches 15; Conservative
SOFTWARE: Patentin version 3.1
SEQ ID NO 86807
LENGTH: 18
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ORGANISM: Homo Sapiens
                                                                                              , ORGANISM: Homo sapiens
US-10-310-188-86807
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LENGTH: 18
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APPLICANT: Wyatt, Jacqueline R.
APPLICANT: Wickers, Alexander
APPLICANT: Vickers, Inmothy A.
TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
TITLE OF INVENTION: GENERATION BY OLIGONUCLEOTIDES AND
TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
CURRENT APPLICATION NUMBER: US/10/388,263
CURRENT FILING DATE: 2003-03-12
NUMBER OF SEQ ID NOS: 947
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
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APPLICANT: Sanguinetti, Michael C.
APPLICANT: Curran, Mark E.
APPLICANT: Landes, Gregory M.
APPLICANT: Landes, Gregory M.
APPLICANT: Burn, Timothy D.
APPLICANT: Splawski, 1gor
TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
FILE REPERENCE: 2323-163
CURRENT APPLICATION NUMBER: US/10/368,643
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 09/597,731
PRIOR APPLICATION NUMBER: US 09/135,010
PRIOR APPLICATION NUMBER: US 09/135,010
PRIOR PILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: US 08/921,068
PRIOR FILING DATE: 1998-08-29
PRIOR FILING DATE: 1997-08-29
PRIOR FILING DATE: 1997-08-29
PRIOR FILING DATE: 1995-10-29
PRIOR FILING DATE: 1995-10-29
PRIOR FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PATENTIN VET: 2.0
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0.6%; Score 13.2; DB 1;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3;
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GENERAL INFORMATION
APPLICANT: COWSEIT, LEX M.
APPLICANT: BASET, Brenda F.
APPLICANT: MCNeil, John
APPLICANT: Freier, Susan M.
PROFICANT: Freier, Susan M.
PROFICANT: Preier, Susan M.
PROFICANT: Preier, Susan M.
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US-10-368-643-74
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Matches 15; Conserv
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APPLICANT:
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; LOCATION: (5016571)...(5016588)

; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 55445

US-10-367-832A-51780
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                                                                                                                                                                                                                                                                                                                                     APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/367,832A
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SOFTWARE: Proprietary
SEQ ID NOS: 64158
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US-10-367-922A-60330/c
Sequence 60330 Application US/10367832A
Sequence 60330 Application US/10367832A
GENERAL INPORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT PELLICATION NUMBER: US/10/367,832A
NUMBER OF SEQ ID NOS: 64158
SEQ ID NO 60330
LENGTH: 18
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                  Query Match
0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels
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0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
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83.3%; Pred. No. 6.1e+02;
tive 0; Mismatches 3;
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US-10-367-832A-51780
; Sequence 51780, Application US/10367832A
; GENERAL INFORMATION:
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US-10-367-832A-60330
                                                                                                                1119 GCCCAGTTCCACCTTCAC 1136
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APPLICANT: Keating, Mark T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1120 CCCAGTTCCACCTTCACC 1137
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Best Local Similarity 83.33
Matches 15; Conservative
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US-10-368-643-74
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APPLICANT: Sampson, Addrew Johnson
APPLICANT: Bangson, Addrew Johnson
APPLICANT: Blacker, Deborah Lynne
TITLE OF INVENTION: GENES AND FOLYMORPHISMS ON CHROMOSOME 10
TITLE OF INVENTION: GENES AND FOLYMORPHISMS ON CHROMOSOME 10
TITLE OF INVENTION: GENES AND FOLYMORPHISMS ON CHROMOSOME 10
TITLE OF INVENTION: NUMBER: US/10/600,009
FILE REFERENCE: 37481-3308B
CURRENT FILING DATE: 2003-06-18
FRIOR APPLICATION NUMBER: US 60/339,525
FRIOR APPLICATION NUMBER: US 60/336,929
FRIOR APPLICATION NUMBER: US 60/337,052
FRIOR APPLICATION NUMBER: US 60/338,363
FRIOR APPLICATION NUMBER: US 60/368,919
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                                                                          Length 18;
                                                                                                                              Indels
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                                                                    Score 13.2; DB 1;
Pred. No. 6.1e+02;
0; Mismatches 3;
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83.3%; Pred. No. 6.1e+02;
vative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                RESULT 1038
US-10-600-09-341
is Sequence 341, Application US/10600009
is GENERAL INFORMATION:
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APPLICANT: Becker, Kenneth David
APPLICANT: Velicelebi, Gonul
APPLICANT: Plice, Kathryn J.
APPLICANT: Mang, Xin
APPLICANT: Tanzi, Rudolph E.
                                                                                                                                                                            1020 AGAGGGGAGCTTGAAGG 1037
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Saunders, Aleister J.
Mullin, Kristina M.
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Becker, Kenneth David
APPLICANT: Velicelebi, Gonul
APPLICANT: Blliot, Kathryn J.
APPLICANT: Wang, Xin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18
                                                                    0.6%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                18 AGTGGAGGAGCTTGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ranzi, Rudolph E.
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                                                            Query Match
Best Local Similarity 83.33
Matches 15; Conservative
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Best Local Similarity 83.33
Matches 15; Conservative
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              US-10-423-007-31
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APPLICANT:
APPLICANT:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OFFOWO, TOSHIHIKO
APPLICANT: TSUCHIYA, MASAYUKI
APPLICANT: KOISHIHARA, YASUO
APPLICANT: KOSISHIHARA, YASUO
APPLICANT: KOSISHIHARA, MASAXI
ITILE OF INVENTION: ENOMIC GENE ENCODING HM 1.24 ANTIGEN PROTEIN AND
TITLE OF INVENTION: GENOMIC GENE ENCODING HM 1.24 ANTIGEN PROTEIN AND
TITLE OF INVENTION: PROMOTER THEREOF
FILE REFERENCE: 053466/0285
CURRENT APPLICATION NUMBER: US/09/622,166A
PRIOR APPLICATION NUMBER: US/09/622,166A
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-03-24
FRIOR RILING DATE: 1998-03-24
NUMBER OF SEQ ID NOS: 33
SSOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wyatt, Jeagueline R.
APPLICANT: Borchers, Alexander
APPLICANT: Borchers, Timothy A.
TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
TITLE OF INVENTION: GENERATION BY OLIGONUCLEOTIDES AND
TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
FILLS PERRENCE: ISIS-4503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/388,263
CURRENT FILING DATE: 2003-03-12
NUMBER OF SEQ ID NOS: 947
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 18
                                                                                                                                                                                       Sequence 221, Application US/10388263 GENERAL INFORMATION:
1006 TCGACACCTGAAAAAGAG 1023
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                                                      18 TAGACACCTGGAACAGAG 1
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Sasmor, Henri M.
Brooks, Douglas G.
Ohashi, Cara
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                                                                                                                                                                                                                                                                           Baker, Brenda F.
McNeil, John
                                                                                                                                                                                                                                              APPLICANT: Cowsert, Lex M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 15; Conserv
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APPLICANT:
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Sequence 355, Application US/09949427

Sequence 355, Application US/09949427

GENERAL INFORMATION:
APPLICANT: Bodnar, Jackie S.
APPLICANT: Castellani, Lawrence W.
APPLICANT: Castellani, Lawrence W.
APPLICANT: Chatterjee, Aurobindo
APPLICANT: Chatterjee, Aurobindo
APPLICANT: Lusis, Aldons J.
APPLICANT: David
APPLICANT: David
APPLICANT: Ross, David
APPLICANT: Ross, David
APPLICANT: Wu, Chenyan
ITITLE OF INVENTION: Gene and Sequence Variation Associated with Cancer
FILE REFERENCE: 02810.0014.NBUSG2
CURRENT PAPLICATION NUMBER: US/09/949,427
FILE REFERENT FILING DATE: 2001-09-07
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 405
SOFTWARE: PatentIn version 3.1
SEQ ID NO 355
LENGTH: 21
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APPLICANT: Bodnar, Jackie S.
APPLICANT: Catellani, Lawrence W.
APPLICANT: Catellani, Lawrence W.
APPLICANT: Charter-lec, Aurobindo
APPLICANT: Charter-lec, Aurobindo
APPLICANT: Lusis, Aldons J.
APPLICANT: David
APPLICANT: Taturi, Sherrie
APPLICANT: Wu, Chenyan
TILE OF INVENTION: Gene and Sequence Variation Associated with Cancer; FILE REFERENCE: 8038 02810-0014
CURRENT APPLICATION NUMBER: US/09/949,427A
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 415
SOFTWARE: PatentIn version 2.1
SEQ ID NO 355
LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Synthetic Primer US-09-949-427-355
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1020 AGAGGGGGAGCTTGAAGG 1037
                                                                        1 AGAGGAGGAGTTTGATGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 GGAGCCTCAGTCCAGAGA 53
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US-09-949-427-355/c
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Blumenfeld, Marta
APPLICANT: Blabelle
ITILE OF INVENTION: BIALLELIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY...
FILE REFERENCE 8 44.021.PRO
CURRENT APPLICATION NUMBER: US/60/216,745
CURRENT FILING DATE: 2000-06-30
SOFTWARE: Patent.pm
SEQ ID NO 8632
LENGTH: 18
TUDENTALE PATENT FILING DATE: DA
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; LOCATION: 1..18
: OTHER INFORMATION: upstream amplification primer 99-31024 for SEQ 4101,
US-60-216-745-8632
    APPLICANT: Saunders, Aleister J.
APPLICANT: Saunders, Aleister J.
APPLICANT: Saunders, Aleister J.
APPLICANT: Saunders, Aleister J.
APPLICANT: Saunders, Aleister J.
APPLICANT: Blacker, Andrew Johnson
APPLICANT: Blacker, Deborah Lynne
ITILE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
ITILE OF INVENTION: ASSOCIATED WITH ALZHITMER'S DISEASE AND OTHER
ITILE OF INVENTION: NEURODERSENATIVE DISEASES
TITLE OF INVENTION: NEURODERSENATIVE DISEASES
TITLE OF INVENTION: NEURODERSENATIVE DISEASES
CURRENT APPLICATION NUMBER: US/10/600,009
CURRENT FILING DATE: 2001-10-025
PRIOR FILING DATE: 2001-11-08
PRIOR PILING DATE: 2001-11-08
PRIOR PELING DATE: 2001-11-08
PRIOR PELING DATE: 2001-11-09
PRIOR PELICATION NUMBER: US 60/336,929
PRIOR FILING DATE: 2001-11-09
PRIOR PELING DATE: 2001-12-04
PRIOR PELING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 564
SEC ID NO 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 83.3
Matches 15; Conservative
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Best Local Similarity 83.3
Matches 15; Conservative
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ORGANISM: Homo Sapiens
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LENGTH: 18
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Length 21;

DB 1;

0.6%; Score 13.2;

Query Match

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US-60-353-987-560795
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CURRENT APPLICATION NUMBER: 0.014.WUSER: 0.014.WUSER: 0.014.WUSER: 0.014.WUSER: 0.0014.WUSER: 0.0014.WU
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US-10-355-577-560795
US-10-355-577-560795
Sequence 560795, Application US/10355577
GENERAL INFORMATION:
APPLICANT: Mitthann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
FILE REFERENCE: 3121
CURRENT APPLICANT: O030-01-31
CURRENT FILING DAID: NUMBER: US/10/355,577
SOURENT FILING DAID: 2003-01-31
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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83.3%; Pred. No. 7.8e+02;
iive 0; Mismatches 3; Indels
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                                         Indels
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Pred. No. 7e+02;
0; Mismatches
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Sequence 355, Application US/09949428
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Synthetic Primer US-09-949-428-355
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bodnar, Jackie S.
APPLICANT: Castellani, Lawrence W.
APPLICANT: Chatterjee, Aurobindo
APPLICANT: de Jong, Pieter
APPLICANT: Lusis, Aldons J.
APPLICANT: Ohmen, Jeff
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   Best Local Similarity 83.3%; Pr
Matches 15; Conservative 0;
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                                                                                                              36 GGAGCCTCAGTCCAGAGA 53
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Best Local Similarity 83.3
Matches 15; Conservative
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CORGANISM: Homo sapien
US-10-355-577-560795
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Matches 15, Conserv
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APPLICANT:
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RESULT 1045

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Gaps
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) Sequence 4, Application US/08529190A
) GENERAL INFORMATION:
| APPLICANT: Magneci, Maria G. |
| TITALE OF INVENTION: CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM
| NUMBER OF SEQUENCES: 63
| CORRESPONDENCE ADDRESS:
Sequence 560795, Application US/60353987
GENERAL INFORMATION:
APPLICANT: Mitteman, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
FILE REFERENCE: 3121
CURRENT PELLING NUMBER: US/60/353,987
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 560795
LENGTH: 25
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OPERATING SYSTEM: DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,190A
FILING DATE: 15-SEP-1995
CLASSIFICATION 5T4
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen A
REGISTRATION UNBER: 34,380
REFERENCE/DOCKET NUMBER: THERE-005AX
TELECOMMUNICATION INFORMATION:
TELEFHONE: 617-245-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Banner & Allegretti
STREET: 75 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                          2075 ACTGTCCTAAGGCAGGG 2092
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                                                                                                                                                                                                                                                                                                                                                                                             15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 base pairs nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-345-9111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapien
US-60-353-987-560795
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Matches 15; Conserv
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Masucci, Maria G.
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                                                                                                                                                                                     USA
                                                                                                                                                                                  COUNTRY: U
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                                                                                                                                                                                                                                                                                   APPLICANT: Masucci, maria G.
TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES CONFERRING
TITLE OF INVENTION: INVISIBILITY TO THE IMMONE SYSTEM.
NUMBER OF SEQUENCES: 123
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathleen M. Williams, Banner & Witcoff, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.6%; Score 13; DB 1; Length 24; Best Local Similarity 76.2%; Pred. No. 8e+02; Matches 16; Conservative 0; Mismatches 5; Indels
    0.6%; Score 13; DB 1; Length 24; 76.2%; Pred. No. 8e+02; cive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Wordperfect 6.1a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/733,369A FILING DATE: 17 October, 1996 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/522,995 FILING DATE: 01-SEP-1995 PRIOR APPLICATION DATA: US 08/529,190 FILING DATE: 15-SEP-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: SE 95013249 FILING DATE: 10-APR-1995 PRIOR APPLICATION NUMBER: SP 95013249 FILING DATE: 10-APR-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/GB96/00876
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ATTORNEY/AGENT INFORMATION:
NAME: Williams, Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 95-1391-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEPAX: 617-345-9101
                                                                                                                                                                                                RESULT 1047
US-08-733-369A-60/c
; Sequence 60, Application US/08733369A
; GENERAL INFORMATION:
                                                                                         296 TGCTCCTGGAGCTGTTGGTGG 316
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 bases
Query Match
Best Local Similarity 76.2<sup>3</sup>
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: Massachusetts
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STRANDEDNESS: single
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; Sequence 55, Application US/08970900; GENERAL INFORMATION:

RESULT 1048 US-08-970-900-55/c

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| LOCATION: (437846)...(437861)
| OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 40:
PCT-US02-25940-3485
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SERERAL INFORMATION:
APPLICANT Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmi, FILE REFERBNCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PCT/US02/25940
CURRENT FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 25502
SOFTWARE: Proprietary
SOFTWARE: Proprietary
SEQ ID NO 3485
LENGTH: 16
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     FUSION PROTEINS HAVING INCREASED HALF-LIVES
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0.6%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmi
                                                                              Kathleen M. Williams, Banner & Witcoff, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 24;
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                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13; DB 1;
Pred. No. 8e+02;
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                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Wordperfect 6.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,900
FILING DATE: 14-NOV-1997
PR.OR APPLICATION NUMBER: US 60/030,986
FILING DATE: 15-NOV-1996
FILING DATE: 15-NOV-1996
FILING DATE: 25-UN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Williams, Kathleen M.
REGISTRATION NUMBER: 34,380
REFERNICE/DOCKET NUMBER: 3255/59831
TELECOMMINICATION INFORMATION:
TELEPHONE: 617-345-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: other nucleic acid
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TITLE OF INVENTION: FUSION PROTE NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS: ADDRESSE Kathleen M. William STREET: One Financial Center CITY: Boston STATE: Massachusetts
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Best Local Similarity 76.2%;
Matches 16; Conservative C
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INFORMATION FOR SEQ ID NO: 55
SEQUENCE CHARACTERISTICS:
'RUGTH: 24 bases
'RUGTH: 24 bases
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STRANDEDNESS: single
TOPOLOGY: linear
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schultz451-1.rnpm

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                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08529190A
GENERAL INFORMATION:
APPLICANT: Masucci, Maria G
TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES
TITLE OF INVENTION: CORPERRING INVISIBILITY TO THE IMMUNE SYSTEM
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                             0.6%; Score 12.8; DB 1;
87.5%; Pred. No. 6.9e+02;
tive 0; Mismatches 2;
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70.8%; Pred. No. 8.5e+02;
iive 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: THERE-005AX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,190A
FILING DATE: 15-SEP-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 GIGCICCIGGAGCIGITGGIGGGA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ph.D., Kathleen A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 Gregageregasereceeredaa 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Banner & Allegretti
STREET: 75 State Street
                                                                                                                                                                                                                                                                   1380 GCGCCCTAGGCCTG 1395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 617-345-9100
                           SOFTWARE: Patentin version 3.1 SEQ ID NO 35499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                             16 ecedecedededere 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: Genomic DNA HYPOTHETICAL: NO
                                                                                                                                                                               Query Match 0.6'
Best Local Similarity 87.5'
Matches 14; Conservative
      NUMBER OF SEQ ID NOS: 86841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 617-345-91
TELEFAX: 617-345-9111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: sing
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Best Local Similarity
Matches 17; Conserv
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STREET: 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE:
ORIGINAL SOURCE:
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                                                                                                                                      US-10-310-188-35499
                                                                                                                                                                                                                                                                                                                                                                          RESULT 1053
US-08-529-190A-7/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 02109
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                                                                        LENGTH: 18
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US-10-110-188-35499/c
US-10-110-189-35499/c
Sequence 35499/s Application US/10310188
GENERAL INFORMATION:
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4094
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OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber =
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TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmi
FILE REPERENCS: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/227,563
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 25502
SEQ ID NO 3485
LENGTH: 16
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APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmi
FILE REFERENCE: Jun Segeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/367,892
CURRENT FILING DATE: 2003-03-06
NUMBER OF SEQ ID NOS: 25502
SOFTWARE: Proprietary
SEQ ID NO 3485
LENTH: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Deinococcus radiodurans Rl complete genome, Plasmi
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87.5%; Pred. No. 6.3e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (437846)...(437861)
OTHER INFORMATION: Chromosome = 1 Strand = negative
                                                                                                                             US-10-227-563-3485/c; Sequence 3485, Application US/10227563; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3485, Application US/10367892
GENERAL INFORMATION:
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1380 GCGCCCCTAGGCTG 1395
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                                             16 GCGGCGGCGAGGGCTG 1
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Best Local Similarity 87.5
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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APPLICANT: Becker, Kenneth David
APPLICANT: Welicelebi, Gonul
APPLICANT: Welicelebi, Gonul
APPLICANT: Welicelebi, Gonul
APPLICANT: Wellock Kathryn J.
APPLICANT: Tanzi, Rudolph E.
APPLICANT: Tanzi, Rudolph E.
APPLICANT: Bartram, Lars
APPLICANT: Bartram, Lars
APPLICANT: Bancher, Aleister J.
APPLICANT: Bancher, Aleister J.
APPLICANT: Blacker, Deborah Lynne
APPLICANT: Blacker, Deborah Lynne
TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE
FILE REPERENCE: 37481-3308PC
CURRENT APPLICATION NUMBER: PS 60/339,525
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.6%; Score 12.8; DB 1; Length 24; Best Local Similarity 70.8%; Pred. No. 8.5e+02; Matches 17; Conservative 0; Mismatches 7; Indels
                                                                                   Diskette, 3.50 inch, 1.44 Mb storage
                                                                                                                                                                 CURBATA PRELICATION DATA:

CURBATA APPLICATION DATA:

APPLICATION NUMBER: US/08/970,900
FILING DATE: 14-NOV-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/030,986
FILING DATE: 15-NOV-1996
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/048,945
FILING DATE: 25-UN-1997
ATTORNEY/AGENT INFORMATION:

NAME: Williams, Kathleen M.

REGISTRATION NUMBER: 34,380

REFERENCE/DOCKET NUMBER: 3255/59831
TELECOMMONICATION INFORMATION:

TELECOMMONICATION INFORMATION:

TELEFRAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 bases

TYPE: mucleic acid

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 GIGCICCIGGAGCIGITGGIGGGA 318
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                          ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inct
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) MOLECULE TYPE: other nucleic acid US-08-970-900-57
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  COUNTRY:
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GENERAL INFORMATION:
APPLICATT Masucci, Maria G.
TITLE OF INVENTION: FUSION PROTEINS HAVING INCREASED HALF-LIVES.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Actible M. Williams, Banner & Witcoff, Ltd.
STREET: One Financial Center
RESULT 1054
US-08-733-369A-63/c
; Sequence 63, Application US/08733369A
; GENERAL INFORMATION:
GENERAL INFORMATION:
; TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES CONFERING
; TITLE OF INVENTION: INVISIBILITY TO THE IMMUNE SYSTEM:
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathleen M. Williams, Banner & Witcoff, Ltd.
STREET: One Financial Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER. IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,369A
FILING DATE: 17 October, 1996
FILING DATE: 10.0ctober, 1996
FILING DATE: 01.5EP-1995
FILING DATE: 01.5EP-1995
FILING DATE: 15.5EP-1995
FILING DATE: 15.5EP-1995
FILING DATE: 15.5EP-1995
FILING DATE: 10.APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Williams, Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 95-1391-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 GIGCTCCTGGAGCTGTTGGTGGGA 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 24 bases
LENGTH: mucleic acid
STRANDEDNESS: single
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Best Local Similarity
Matches 17; Conserva
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US-08-970-900-57/c
                                                                                                                                                                                                                                                                                                                                                                STATE: Mass
COUNTRY: US
ZIP: 02111
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STATE:
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APPLICANT:
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APPLICANT:
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APPLICANT: Mullin, Kristina M.

APPLICANT: Sampson, Andrew Johnson

APPLICANT: Blacker, Deborah Lymne

APPLICANT: Blacker, And Polymone Hymne

TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10

TITLE OF INVENTION: ASSOCIATED WITH ALCHEIMBR'S DISEASE AND OTHER

TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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0.6%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 7.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                     Query Match
0.6%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 7.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US/10/282,174
CURRENT FILING DATE: 2002-10-25
CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: US 60/339,525
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 564
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
NUMBER OF SEQ ID NOS: 564
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 162
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Becker, Kenneth David
APPLICANT: Velicelebi, Gonul
APPLICANT: Biliot, Kathryn J.
APPLICANT: Tanzi, Rudolph E.
APPLICANT: Tanzi, Rudolph E.
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                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                           OTHER INFORMATION: Primer
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                                                                                                              TYPE: DNA
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RESULT 1058 US-10-600-009-162 ; Sequence 162, Application US/10600009

ACTCCAGGCTTCTC 15

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Sequence 30 Application PC/TUS0229102

Sequence 30 Application PC/TUS0229102

GENERAL INFORMATION:
APPLICANT: Applied Biosystems
APPLICANT: Bolchakova, Elema V.
APPLICANT: Rozzelle, James E.
TITLE OF INVENTION: A Novel DNA Polymerase from the Thermophilic Thermus Scotoductu
FILE REFERENCE: 1560.002W01

CURRENT APPLICATION NUMBER: PCT/US02/29102

CURRENT FILING DATE: 2002-09-13

PRIOR APPLICATION NUMBER: US 60/334489

PRIOR APPLICATION NUMBER: US 60/332218

PRIOR FILING DATE: 2000-11-4

NUMBER OF SEQ ID NOS: 50

SOFTWARE FRESEE for Windows Version 4.0

SEQ ID NO 30

LENGTH: 17
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APPLICANT: Blacker, Deborah Lynne
TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                  TILLE CF INVENTION: NEURODEGENERATIVE DISEASE CURRENT APPLICATION NUMBER: US/10/600,009 CURRENT FILING DATE: 2003-06-18 CURRENT FILING DATE: 2003-06-18 PRIOR APPLICATION NUMBER: US 60/339,525 PRIOR APPLICATION NUMBER: US 60/338,010 PRIOR FILING DATE: 2001-10-25 PRIOR PRILING DATE: 2001-11-08 PRIOR FILING DATE: 2001-11-08 PRIOR FILING DATE: 2001-11-09 PRIOR FILING DATE: 2001-11-09 PRIOR FILING DATE: 2001-11-09 PRIOR FILING DATE: 2001-11-09 PRIOR FILING DATE: 2001-12-04 PRIOR FILING DATE: 2001-12-04 PRIOR PILING DATE: 2001-12-04 PRIOR FILING DATE: 2002-03-28 PRIOR FILING DATE: 2002-03-28 PRIOR FILING DATE: 2002-10-25 NUMBER OF SEQ ID NOS: 564 SOFTWARE FALING DATE: 2002-10-25 NUMBER OF SEQ ID NOS: 564 LENGTHARE: PASLERQ FOR Windows Version 4.0 SEQ ID NOI 162 LENGTH: 18
Becker, Kenneth David
Velicelebi, Gonul
Blliot, Kathryn J.
Wang, Xin
                                                                                                                                                    Bertram, Lars
Saunders, Aleister J.
Mullin, Kristina M.
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                                                                                                                     Tanzi, Rudolph E.
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; Sequence 51, Application PC/TUS0237657
; GENERAL INFORMATION:
; APPLICANT: APPLERA CORPORATION
; APPLICANT: ROZEELLE, James
; APPLICANT: BOLCHAKOVA, Elema
; TITLE OF INVENTION: THERMUS BROCKIANUS NUCLEIC ACID POLYMERASES
; TITLE REFERENCE: 4768WO
; CURRENT APPLICATION NUMBER: PCT/US02/37657
; CURRENT FILING DATE: 2003-02-24
; PRIOR PLING DATE: 2003-02-24
; PRIOR PLING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PATENTIN VERSION 3.2
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   Length 17;
Ouery Match 0.6%; Score 12.2; DB 1; Length 1
Best Local Similarity 82.4%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels
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Pred. No. 7.9e+02;
0; Mismatches 3;
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ORGANISM: Thermus brockianus
PCT-US02-37657-51
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Best Local Similarity
Matches 14; Conserv
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LENGTH: 17
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US-10-302-817A-51/c; Sequence 51, Application US/10302817A; GENERAL INFORMATION:

RESULT 1062

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APPLICANT: NOZZALIA

APPLICANT: NOZZALIA

TITLE OF INVENTION: THERMUS BROCKIANUS NUCLEIC ACID POLYMERASES

FILE REFERENCE: 4768US

CURRENT APPLICATION NUMBER: US/10/302,817A

CURRENT APPLICATION NUMBER: US/10/302,817A

CURRENT FILING DATE: 2002-11-22

PRIOR PRICATION NUMBER: 60/334,434

PRIOR PILING DATE: 2001-11-30

NUMBER OF SEQ ID NOS: 58

SOFTWARE: Patentin version 3.2

SEQ ID NO 51

LENGTH: 17

TYPE: DNA

ORGANISM: Thermus brockianus
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VS-10-303-109A-30/C

Sequence 30, Application US/10303109A

GENERAL INFORMATION:
APPLICANT: BOLGHAKOVA, Elena
APPLICANT: ROZZELLE, James

TITLE OF INVENTION: Thermus Oshimai Nucleic Acid Polymerases
FILE REFERENCE: 477708

CURRENT APPLICATION NUMBER: US/10/303,109A

CURRENT PILING DATE: 2002-11-22

PRIOR APPLICATION NUMBER: US 60/334,798

PRIOR FILING DATE: 2001-11-30

NUMBER OF SEQ 1D NOS: 39

SEQ 1D NO 30

LENGTH: 17
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Pred. No. 7.9e+02;
0; Mismatches 3; Indels
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0.6%; Score 12.2; DB 1;
Best Local Similarity 82.4%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 3;
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Best Local Similarity
Matches 14; Conserv
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Homo sapiens
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S81271/c
                                                                                                                                                            ORGANISM
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MEDLINE
PUBMED
REMARK
                                                                                                           ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                              REFERENCE
AUTHORS
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               DB
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BD209419
BD209419.1 GI:33019189
Unidentified
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A61K37/66,
        C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
A61K37/66,
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Key Location/Qualifiers
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                                                   Enzymatic nucleic acid treatment of diseases or conditions
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PD 08-MAY-2002
PD 08-MAY-2002
PP 26-APR-1999 US 60/083217,18-SEP-1998 US 60/100842
ES-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A
                                                                                                             organism='Hepatitis virus (hepatitis C
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0.5%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 6.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                            0.5%; Score 10.4; DB 1; Length 14; 91.7%; Pred. No. 6.5e+02; tive 0; Mismatches 1; Indels
                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
                                                                                                                                                       1. .14
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
                                                                             hepatitis C virus infection
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                                                                     related to
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Best Local Similarity 91.77
Matches 11; Conservative
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
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                                                                                                                                                               S81271 14 bp mRNA linear PRI 07-MAY-1993 mitochondrial acetoacetyl-coenzyme A thiolase [human, mRNA Partial
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 14)

Fukao,T., Yamaguchi,S., Orii,T., Schutgens,R.B., Osumi,T. and Hashimoto,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 81271] from the original journal article. This sequence comes from Figure 2. exon 8 skipping.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="mitochondrial acetoacetyl-coenzyme A thiolase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
1. .14
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                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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S81271.1 GI:245356
1216 GCTGACCCCATC 1227
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Best Local Similarity 91.7
Matches 11; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model nucleic search, OM nucleic

March 1, 2004, 15:39:29; Search time 0.001 Seconds (without alignments) 1456.514 Million cell updates/sec Run on:

us-09-695-451-1 22,61 Title: Perfect score:

IDENTITY NUC Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

oggeccagtgatettgaace.....tacactaaaattetgaagtt 2161

25 segs, 337 residues Searched:

50 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 8 Maximum DB seq length: 80

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 44 summaries

rnpn.seg:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | ١. | ce | e 2383 | 1271 | e 1272 | 16, | 20, | Sequence 49917, A | Sequence 2689, Ap | Seguence 2689, Ap | Sequence 20, Appl | Sequence 1271, Ap | Sequence 1272, Ap | Sequence 19, Appl | Sequence 19, Appl | Sequence 23, Appl | Sequence 25, Appl | Sequence 80, Appl | Sequence 4, Appli | Sequence 49917, A | Sequence 15, Appl | Sequence 23831, A | Sequence 23832, A | Sequence 6, Appli | 7, | 9 | 7, | equence 38, | 938, | 3 | equence 25, | 10, | ò |
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| SUMMARIES | | US-10-774-118-15 | -10-770-726-238 | 0-726-23 | JS03-31862-12 | 03-31862-12 | 1-480-89-1 | | 7-471-49 | 1 | $^{\circ}$ | US-09-892-360-20 | PCT-US03-31862-1271 | PCT-US03-31862-1272 | US-10-484-991-19 | US-10-484-991-19 | -484- | US-10-484-991-25 | -484-991-8 | 1-451-323-4 | 10-767 | 10-774-118-1 | 38 | -726-2383 | US-10-652-361-6 | -361- | 0-652-43 | 0-652-430- | -10-660-897-3 | US-10-660-897-38 | US-10-484-991-23 | S-10-484-991-25 | r-US03-26191A | US-10-484-991-50 |
| | DB | 1 | - | ~ | Н | Н | Н | Н | Н | Н | | | | | | | | | Н | Н | Н | Н | Н | Н | Н | Н | Н | Н | Н | H | Н | H | Н | Н |
| | Query Match Length | 87 | 21 | 21 | 17 | 17 | 15 | 15 | 16 | 14 | 14 | 15 | 17 | 17 | 12 | 12 | 12 | 12 | 12 | 12 | 16 | 18 | 21 | 21 | 10 | 10 | 10 | 10 | 11 | 11 | 12 | 12 | 12 | 12 |
| οN | Query Match | | 0.7 | | | | | | | | | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | | | | 0.4 | | 0.4 | 0.4 | 0.4 | 0.4 |
| | Score | 18 | 14.8 | 4. | 2 | ς. | Η. | 11.4 | i | | | • | 6 | 6 | | | | | 8.8 | | | | | | 8.4 | 8.4 | 8.4 | 8.4 | 8.4 | 8.4 | 8.4 | 4.8 | 8. | 8.4 |
| | ult No. | 1 | 7 | е | 4 | ហ | 9 | 7 | œ | თ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 59 | 30 | 31 | 32 | 33 |
| | Result No. | ¦ 0 | U | υ | υ | | υ | υ | υ | | υ | | | υ | | υ | υ | | υ | บ | | | | | | O | | ပ | | υ | | υ | υ | U |

| | Sequence 19, Appl Sequence 24, Appl | 32, | 9,79 | Sequence 7, Appli Sequence 6, Appli | Sequence 7, Appli |
|--------------------------------------|--|--------------------------------------|-------------------------------------|--|-------------------|
| US-10-660-897-11 US-10-660-897-11 | US-10-660-897-19 US-10-660-897-24 | US-10-660-897-24 US-10-660-897-32 | US-IU-66U-897-32 US-10-652-361-6 | US-10-652-361-7 US-10-652-430-6 | US-10-652-430-7 |
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ALIGNMENTS

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APPLICANT: Daddona, Peter
APPLICANT: Ghrayeb, John
APPLICANT: Giegel, Scott
TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
TITLE OF INVENTION: Human Tumor Necrosis Factor
TITLE OF INVENTION: Human Tumor Necrosis Factor
FILE, REFERENCE: 0975-1005-038
CURRENT APPLICATION NUMBER: US 09/756,301
PRIOR PRILING DATE: 1998-08-12-11
PRIOR PRILING DATE: 1998-08-12-11
PRIOR APPLICATION NUMBER: U.S. 08/570,674
PRIOR APPLICATION NUMBER: U.S. 08/324,799
PRIOR FILING DATE: 1994-10-04
PRIOR PELING DATE: 1994-02-04
PRIOR FILING DATE: 1993-01-29
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-01-29
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-03
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Sequence 15, Application US/10774118
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
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18 Trerectacccadarr 1 RESULT 2 US-10-770-726-23831/c 셤

835 ITGIGCCIACCCCAGAIT 852

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: UNIVERSITY OF DELAWARE

APPLICANT: WINVERSITY OF DELAWARE

APPLICANT: WINVERSITY OF DELAWARE

APPLICANT: WAN BRABANT, ANJA

TITLE OF INVENTION: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION

TITLE OF INVENTION: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION

TITLE OF INVENTION: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION

FILE REFRENCE: Nabro-18 PCT

CURRENT APPLICATION NUMBER: DCT/US03/31862

CURRENT FILING DATE: 2003-10-07

PRIOR FILING DATE: 2003-03-07

PRIOR PRIOR APPLICATION NUMBER: US 60/416,983

PRIOR PRIOR DATE: 2002-10-07

NUMBER OF SEQ ID NOS: 2707

SOUTHWARE: PALENTIN VERSION 3.2
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GENERAL INFORMATION:
APPLICANT: BURCOGLU, ARSINUR
TITLE OF INVENTION: METHOD OF TREATING HIV INFECTION
AND RELATED SECONDARY INFECTIONS THEREOF
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/768,089
                                                                                                                                                                                                                                                 0.6%; Score 12.2; DB 1;
82.4%; Pred. No. 2.7;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 12.2; DB 1;
Pred. No. 2.7;
0; Mismatches 3;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 02-Feb-2004 CLASSIFICATION: <Unknown>
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          869 CTGAGGACTCAGGCACC 885
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          SOFTWARE: PatentIn version 3.2
SEQ ID NO 1271
LENGTH: 17
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Best Local Similarity 82.4%;
                                                                                                                TYPE: DNA ORGANISM: Triticum aestivum
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; ORGANISM: Triticum aestivum
PCT-US03-31862-1272
                                                                                                                                                                                                                                          Query Match 0.6
Best Local Similarity 82.4
Matches 14; Conservative
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                                                                                                                                                          ; OKGANACA: ___PCT-US03'-31862-1271
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US-10-768-089-16/c
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                                                        APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
TITLE OF INVENTION OF SECULO 1001
TREATION
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GENERAL INFORMATION:
APPLICANT: Wyear Brown, Bugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, COMPOSITION
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT APPLICATION NUMBER: US/10/770,726
NUMBER OF SEQ 1D MOS: 48640
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-USO3-31862-1271/c

Sequence 1271, Application PC/TUSO331862

GENERAL INPORMATION:

APPLICANT: UNIVERSITY OF DELAWARE

APPLICANT: VAN BRABANT, ANJA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN

TITLE OF INVENTION: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION

TITLE OF INVENTION: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION

CURRENT PILITAG DATE: 2003-10-07

PRIOR PLICATION NUMBER: US 60/453,360

PRIOR PELICATION NUMBER: US 60/453,360

PRIOR APPLICATION NUMBER: US 60/416,983

PRIOR PLING DATE: 2003-10-07

NUMBER OF SEQ ID NOS: 2707
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88.9%; Pred. No. 0.51;
ative 0; Mismatches 2; Indels
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88.9%; Pred. No. 0.51;
tive 0; Mismatches 2; Indels
Sequence 23831, Application US/10770726
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Best Local Similarity 88.9°
Matches 16; Conservative
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Best Local Similarity 88.9%
Matches 16; Conservative
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US-10-770-726-23832/c
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US-10-770-726-23832
                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 23831
LENGTH: 21
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1.ENGTH: 21
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APPLICANT: WINTERSTIY OF DELAWARE
APPLICANT: WAN BRABANT, ANJA
APPLICANT: WAN BRABANT, ANJA
APPLICANT: WAN BRABANT, ANJA
APPLICANT: WAN BRABANT, ANJA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN
TITLE OF INVENTION: OLIGONUCLECTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION
FILE REPERRENCE: NaPro-18 PCT
CURRENT APPLICATION NUMBER: 2003-10-07
PRIOR APPLICATION NUMBER: US 60/453,360
PRIOR APPLICATION NUMBER: US 60/453,360
PRIOR FILING DATE: 2002-10-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2689, Application PC/TUS0331862
Sequence 2689, Application PC/TUS0331862
GENERAL INFORMATION:
APPLICANT: WILE ERIC B.
APPLICANT: WHICE, ERIC B.
TITLE OF INVENTION: MISHADAY. ANJA
TITLE OF INVENTION: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION
TITLE OF INVENTION NUMBER: PCT
CURRENT APPLICATION NUMBER: US 60/453,360
PRIOR PILING DATE: 2003-03-07
PRIOR PILING DATE: 2002-07-07
PRIOR PILING DATE: 2002-07-07
PRIOR PILING DATE: 2002-10-07
                                                                                                                                                                                                                                                                                                            Length 16;
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Pred. No. 12;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                    ed. No. 5.5;
Mismatches
                                                                                                                                                                                                                                                                                                            Score 11.2;
Pred. No. 5.5
                       FILE:PREFERENCE: CL001505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 49917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2689, Application PC/TUS0331862; GENERAL INFORMATION:
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Best Local Similarity 81.2%;
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LENGTH: 14
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SOFTWARE: Patentin version 3.2
SEQ ID NO 2689
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CORGANISM: Homo sapiens
US-10-767-471-49917
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Best Local Similarity
Matches 11; Conserv
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GENERAL INFORMATION:
APPLICANT: LAZDUNSKI, MICHEL
APPLICANT: LEADUNSKI, MICHEL
APPLICANT: LEADUNSKI, MICHEL
APPLICANT: LEADUNSKI, MICHEL
APPLICANT: ROMEY, GEORGES
ITILE OF INVENTION: HUMAN TERK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE
ITILE OF INVENTION: RILUZOLE
ITILE OF INVENTION: RILUZOLE
ITILE OF INVENTION: RILUZOLE
ITILE OF INVENTION: RILUZOLE
ITILE OF INVENTION NUMBER: US/09/892,360
CURRENT APPLICATION NUMBER: US/09/892,360
CURRENT APPLICATION NUMBER: 60/214,559
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 15
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103-107-671-471-49917/c
5 Sequence 49917, Application US/10767471
6 GENERAL INFORMATION:
7 APPLICANT: CARGILL, Michele et al.
7 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
                                                                                                                                                                                                                                               NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 02939.04541
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9100
               APPLICATION NUMBER: US/09/754,066
FILING DATE: 05-Jan-2001
APPLICATION NUMBER: 08/848,013
FILING DATE: 2001-05-07
APPLICATION NUMBER: 07/830,886
FILING DATE: 04-FEB-1992
APPLICATION NUMBER: 07/748,277
FILING DATE: 21-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-768-089-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 15 base pairs
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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PRIOR APPLICATION DATA:
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 12; Conserv
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US-09-892-360-20/c
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RESULT 13

PCT-US03-31862-1272/c

SEQUENCE 1272, Application PC/TUS0331862

GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF DELAWARE
APPLICANT: WAINC, ERIC B.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN
FILE REFERENCE: NAPLO-18 PCT
CURRENT APPLICATION NUMBER: PCT/US03/31862

CURRENT FILING DATE: 2003-10-07

PRIOR FILING DATE: 2003-03-07

PRIOR FILING DATE: 2003-01-07

NUMBER OF SEQ ID NOS: 2707

SOFTWARE: PALENTIN VERSION 3.2

LENGTH: 17

LENGTH: 17
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APPLICANT: Puri, Raj K.
APPLICANT: Puri, Raj K.
APPLICANT: Rawakami, Koji
APPLICANT: Shii, Ken J.
APPLICANT: Oshi, Bhazat H.
TITLE OF INVENTION: USE OF STERICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY
TITLE OF INVENTION: DELIVER CPG OLIGONUCLEOTIDES IN VIVO
TITLE OF INVENTION: DELIVER CPG OLIGONUCLEOTIDES IN VIVO
CURRENT APPLICATION NUMBER: US/10/484,991
CURRENT APPLICATION NUMBER: US 60/308,283
PRIOR PILING DATE: 2002-07-27
PRIOR APPLICATION NUMBER: PCT/US02/24235
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-29
PRIOR FILING BATE: 2002-07-29
PRIOR FILING PATE: 9002-07-29
PRIOR FILING PATE: 9002-07-29
PRIOR FILING PATE: 9002-07-29
PRIOR FILING PATE: 2002-07-29
PRIOR FILING PATE: 2002-07-29
PRIOR FILING PATE: 2002-07-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 19, Application US/10484991; GENERAL INFORMATION:
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                   864 GGGCACTGAGGACTCAG 880
                                                             1 GGCGACTGAGTCGTCAG 17
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Gursel, Ihsan
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Matches 12; Conserv
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APPLICANT:
APPLICANT:
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LENGTH: 12
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GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF DELAWARE
APPLICANT: KMIEC, ERIC B.
APPLICANT: WAN BRABANT, ANJA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN
FILLE REFERENCE: NAPro-18 PCT
CURRENT APPLICATION NUMBER: PCT/US03/31862
CURRENT FILLING DATE: 2003-10-07
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATIONSI,
APPLICANT: LAZDUNSI,
APPLICANT: LAZDUNSI,
APPLICANT: LESAGE, FLORIAN
FAPLICANT: LESAGE, FLORIAN
FILLE OF INVENTION: HUMAN TREK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE
TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND
TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND
TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND
TITLE OF INVENTION: LIJUZOLE
FILE REFERENCE: 1256-R-00
CURRENT APPLICATION NUMBER: US/09/892,360
CURRENT FILING DATE: 2001-06-27
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 20
LENGTH: 15
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                                                                                                               DB 1;
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Pred. No. 32;
0; Mismatches
                                                                                                                                                           Mismatches
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                                                                                                            0.4%; Score 9.2; Di
78.6%; Pred. No. 19;
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/09892360 GENERAL INFORMATION:
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Best Local Similarity 70.6
Matches 12; Conservative
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                                                                                                               Query Match 0.4
Best Local Similarity 78.6
Matches 11; Conservative
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US-09-892-360-20
                   TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 11; Conserv
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LENGTH: 17
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US-09-892-360-20
LENGTH: 14
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APPLICANT: Ishii, Ken J.
APPLICANT: Ishii, Ken J.
APPLICANT: Ishii, Ken J.
APPLICANT: Ishii, Ken J.
APPLICANT: Uoshi, Bharat H.
TITLE OF INVENTION: DELIVER COF STREICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY
TITLE OF INVENTION: DELIVER COF OLIGONUCLEOTIDES IN VIVO
FILE REFRENCE: 4239-67620
CURRENT APPLICATION NUMBER: US/10/484,991
CURRENT FILING DATE: 2004-01-26
PRIOR FILING DATE: 2004-07-27
PRIOR FILING DATE: 2002-07-29
NUMBER OF SEQ ID NOS: 96
SEQ ID NOS: 96
SEQ ID NO 25
LENGTH: 12
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APPLICANT: IShii, Kan J.
TITLE OF INVENTION: USE OF STERICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY
TITLE OF INVENTION: DELIVER CPG OLIGONUCLEOTIDES IN VIVO
FILE REFERENCE: 4239-67620
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Pred. No. 16;
0; Mismatches 2; Indels
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                                                                FEATURE:
; OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-484-991-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTHER INFORMATION: CpG oligodeoxynucleotide US-10-484-991-25
                                                                                                                                                                                                                                                                                                                                                                                                               Application US/10484991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 80, Application US/10484991 GENERAL INFORMATION:
                                                                                                                                                             0.4%;
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Gursel, Ihsan
                          TYPE: DNA ORGANISM: Artificial Sequence
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Gursel, Ihsan
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Best Local Similarity 83.33
Matches 10; Conservative
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Kawakami, Koji
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Kawakami, Koji
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LENGTH: 12
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APPLICANT:
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APPLICANT:
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APPLICANT: Puri, Raj K.
APPLICANT: Rawakami, Koji
APPLICANT: Ishii, Ken J.
APPLICANT: Ishii, Ken J.
APPLICANT: Ishii, Ken J.
APPLICANT: Joshi, Bharat H.
TITLE OF INVENTION: USE OF STERICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY
TITLE OF INVENTION: DELIVER CPG OLIGONUCLEOTIDES IN VIVO
TITLE OF INVENTION: DELIVER CPG OLIGONUCLEOTIDES IN VIVO
CURRENT FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: US 60/309,283
PRIOR APPLICATION NUMBER: PCF/USO2/24235
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-29
NUMBER OF SEQ ID NOS: 96
SOSPIWARE: PATENTIN VERSION 3.2
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                                                                                                                                                                                                                                                      THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
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    2; Indels
    0; Mismatches
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PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: PCT/US02/24235
PRIOR FILING DATE: 2002-07-29
NUMBER OF SEQ ID NOS: 96
SOFTWARRE: Patentin version 3.2
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23, Application US/10484991 GENERAL INFORMATION:
                                                                                                                                                                                                         ; Sequence 19, Application US/10484991; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Gursel, Ihsan
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Gursel, Ihsan
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Puri, Raj K.
Kawakami, Koji
Ishii, Ken J.
Joshi, Bharat H.
                                               1083 TCCAGGCTTCAC 1094
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    10; Conservative
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Best Local Similarity
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US-10-484-991-19/c
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APPLICANT: Daddona, Peter
APPLICANT: Ghrayeb, John
APPLICANT: Ghrayeb, John
APPLICANT: Siegel, Scott
TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
TITLE OF INVENTION: Anti-TNF Antibodies
CURRENT FILING DATE: 2004-02-06
PRIOR PILING DATE: 2004-01-08
PRIOR PILING DATE: 1994-01-18
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1994-02-04
PRIOR PILING DATE: 1994-02-04
PRIOR PILING DATE: 1994-02-04
PRIOR PILING DATE: 1994-02-04
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PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1993-02-02
PRIOR PILING DATE: 1993-02-03
PRIOR FILING DATE: 1993-02-03
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22.10-770-726-23831
; Sequence 23831, Application US/10770726
; GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Le, Junming
APPLICANT: Vilcek, Jan
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                                                                                                                            Query Match 0.4%;
Best Local Similarity 83.3%;
Matches 10; Conservative
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-767-471-49917
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEDWATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOLSOS
CURRENT PELLORION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 49917
LENGTH: 16
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Sequence 4, Application US/10451323
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MACHAEL,
APPLICANT: PESCHER, PASCALE
TITLE OF INVERTION: INMUNOGENIC GLYCOPEPTIDES, SCREENING, PREPARATION AND USES
FILE REFERENCE: 2382180150PCT
CURRENT APPLICATION NUMBER: US/10/451,323
CURRENT FILING DATE: 2004-01-20
PRIOR APPLICATION NUMBER: FR 00/16808
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
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0.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.4%; Score 8.8; DB 1; Length 12; Best Local Similarity 83.3%; Pred. No. 16; Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: CpG oligodeoxymucleotide US-10-484-991-80
CURRENT APPLICATION NUMBER: US/10/484,991
CURRENT FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: US 60/308,283
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-29
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin version 3.2
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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US-10-767-471-49917
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US-10-451-323-4/c
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LENGTH: 12
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APPLICANT: BAHATT. DAR
APPLICANT: SHARAF, MUHAMAD A.
APPLICANT: SHARAF, MUHAMAD A.
APPLICANT: LIU, TIMOTHY Z.
APPLICANT: LIU, TIMOTHY Z.
APPLICANT: CONNELL, CHARLES R.
APPLICANT: CONNELL, CHARLES R.
APPLICANT: HYLDIG-NIELERN, JERS J.
APPLICANT: APPLICANT AND AND KITS
FILE REFERENCE: 502 US
CURRENT FILING DATE: 2003-08-29
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET: 3.2
SSEQ ID NO S.
LENGTU . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SHARAF, MINAMAD A.
APPLICANT: SHARAF, MINAMAD A.
APPLICANT: LIU TIMOTHY Z.
APPLICANT: LIU TIMOTHY Z.
APPLICANT: CONNELL, CHARLES R.
TILLE OF INVENTION: COMPOSITIONS, METHODS, AND KITS FOR ASSEMBLING PROBES FILE REPRENCE: 5049 US
CURRENT APPLICATION NUMBER: US/10/652,361
CURRENT FILING DATE: 2003-08-29
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATCHIN VET: 3.2
SEQ ID NO 7.
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7. OTHER INFORMATION: Description of Artificial Sequence: Synthetic
7. OTHER INFORMATION: Oligonucleotide
US-10-652-430-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: oligonucleotide
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-652-361-6
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                                                                                                                     Length 10;
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                                                                                                                   Score 8.4; DB 1;
Pred. No. 12;
0; Mismatches 1
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GENERAL INFORMATION:
APPLICANT: WOUDENBERG, TIMOTHY M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAHATT, DAR
SHARAF, MUHAMMAD A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                     Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
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Best Local Similarity
Local 9; Conserva
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APPLICANT: Wyeth
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
TITLE OF INVENTION NUMBER: US/10/770,726
CURRENT APPLICATION NUMBER: US/10/770,726
SURMERNT PILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: PATENTIN VETSION 3.2
LENGTH: 21
                       APPLICANT: Liu, Wei Transport Compositions and Methods for Diagnosing, Preventing, and Treating Title OF INVENTION: Compositions and Methods for Diagnosing, Preventing, and Treating File Reference: Amiolog (031896-010000)
FILE REFERENCE: Amiolog (031896-010000)
FURRENT PILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
LENGTH: 21
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MUDENBERG, TIMOTHY M.
APPLICANT: BENEATT, DARA
APPLICANT: BENEATT, DARA
APPLICANT: BENEATT, DARA
APPLICANT: LIU, TIMOTHY Z.
APPLICANT: LIU, TIMOTHY Z.
APPLICANT: ENARAKOV, SERGUEN
APPLICANT: ENARAKOV, SERGUEN
APPLICANT: CONNELL, CHARLES R.
TITLE OF INVENTION: COMPOSITIONS, METHODS, AND KITS FOR ASSEMBLING PROBES
CURRENT APPLICATION NUMBER: US/10/652,361
CURRENT FILING DATE: 2003-08-29
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 3.2
SEQ ID NO 6
LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 23832, Application US/10770726; GENERAL INFORMATION:
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       Brown, Eugene
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CORGANISM: Homo sapiens
US-10-770-726-23831
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Best Local Similarity
Matches 9; Conserv
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Matches 11; Conserv
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; ORGANISM: RNAi
US-10-770-726-23832
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US-10-770-726-23832
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SERRAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
APPLICANT: HUMAN SERVICES
APPLICANT: HUMAN SERVICES
APPLICANT: Klinman, Dennis M.
APPLICANT: Klinman, Dennis M.
APPLICANT: Bain, Kan J.
APPLICANT: Bain, Kan J.
APPLICANT: Ishii, Ken J.
APPLICANT: Usan SE OF STERICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY
TITLE OF INVENTION: UNBER: US/10/484,991
CURRENT APPLICATION NUMBER: US 60/308,283
FRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: PCT/US02/24235
PRIOR FILING DATE: 2002-07-29
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 23
ILENGTH: 12
                                                                                                                                                                                                                           APPLICANT: Chung, Mary
APPLICANT: Siddiqui-Jain, Adam
APPLICANT: Siddiqui-Jain, Adam
APPLICANT: Whitten, Jeffrey
APPLICANT: Whitten, Jeffrey
APPLICANT: Whitten, Jeffrey
APPLICANT: Whitten, Jeffrey
APPLICANT: Farrell, Thomas
TITLE OF INVENTION: QUADNUPLEX FORMING NUCLEIC ACIDS AND MODULATORS THEREOF
FILE REFERENCE: 532232000800
CURRENT APPLICATION NUMBER: US/10/660,897
CURRENT APPLICATION NUMBER: 60/410,475
PRIOR FILING DATE: 2002-09-12
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 11
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Indels
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; OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-484-991-23
  Mismatches
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GENERAL INFORMATION:
APPLICANT: Jin, Cheng
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Best Local Similarity 90.0.
Local 9, Conservative
  9; Conservative
                                            1859 GAGGATGAGG 1868
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    Matches
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GENERAL INFORMATION:
APPLICANT: Jin, Cheng
APPLICANT: Chung, Mary
APPLICANT: Chung, Mary
APPLICANT: Saididqui-Jain, Adam
APPLICANT: Whitten, Jeffrey
APPLICANT: Farrell, Thomas
APPLICANT: Farrell, Thomas
APPLICANT: FARRELL, THOMAS
APPLICANT: Whitten, USFARRED FOR IDENTIFYING
TITLE OF INVENTION: QUADRUPLEX FORMING NUCLEIC ACIDS AND MODULATORS FILE REFERENCE: 532232000800
CURRENT APPLICATION NUMBER: US/10/660,897
CURRENT FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: 60/410,475
PRIOR FILING DATE: 2002-09-12
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APPLICANT: BAHATY, DAR
APPLICANT: SHARAY, DAR
APPLICANT: SHARAY, MITHAMAD A.
APPLICANT: LIU, TIMOTHY Z.
APPLICANT: LIU, TIMOTHY Z.
APPLICANT: CONNELL, CHARLES R.
APPLICANT: CONNELL, CHARLES R.
APPLICANT: HYLDIG-INELSEN, JENS J.
TITLE OF INVENTION: MULTIPLEX DETECTION COMPOSITIONS, METHODS, AND KITS
FILE REFERENCE: 5023 US
CURRENT FILING DATE: 2003-08-29
NUMBER OF SEQ ID NOS: 33
SOFTWARES PALENTIN Ver. 3.2
SEQ ID NO 7
LENGTH: 10
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                         DB 1; Length 10;
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                         Score 8.4; DB Pred. No. 12; 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 11
                                                                                                                                                                                                                                                                        Sequence 7, Application US/10652430 GENERAL INFORMATION:
APPLICANT: WOUDENBERG, TIMOTHY M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                       0.4%;
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Best Local Similarity 90.0
Matches 9; Conservative
                            Ouery Match
Best Local Similarity 90.0
Matches 9; Conservative
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COTHER INFORMATION: motif US-10-660-897-38
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Best Local Similarity
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APPLICANT: Ishii, Neu Jahappelicant: Ishii, Ren Jahappelicant: Ishii, Ren Jahappelicant: Joshi, Bharat H.
APPLICANT: Joshi, Bharat H.
TITLE OF INVENTION: USE OF STERICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY
TITLE OF INVENTION: DELIVER CPG OLIGONUCLEOTIDES IN VIVO
FILLE OF INVENTION: DELIVER CPG OLIGONUCLEOTIDES IN VIVO
CURRENT APPLICATION NUMBER: US 60/308,283
FRICH REPERSON FOR SECTION ON THE SECTION OF 
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GENERAL INFORMATION:

APPLICANT: Jin, Cheng
APPLICANT: Siddiqui-Jain, Adam
APPLICANT: Siddiqui-Jain, Adam
APPLICANT: Mintten, Jeffrey
APPLICANT: Wintten, Jeffrey
TITLE OF INVENTION: QUARRULEX FORMING NUCLEIC ACIDS AND MODULATORS THEREOF
FILE REFERENCE: 53223200800
FILE REPERENCE: 53223200800
CURRENT FILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-09-12
NUMBER OF SEQ ID NOS: 40

SOFTWARE: FARLSEQ for Windows Version 4.0

LENGTH: 12
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                                                               Gaps
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DB 1; Length 12;
                                                               Indels
                                                                   0; Mismatches
                                 23:
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Score 8.4;
Pred. No. 2
                                                                                                                                                                                                                                                                                         RESULT 33
US-10-484-991-50/c
; Sequence 50, Application US/10484991
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0.4%;
Similarity 90.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klinman, Dennis M.
Gursel, Ihsan
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Kawakami, Koji
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                                                                                                                                  1182 TCCCCGCAGA 1191
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Best Local Similarity
Matches 9; Conserv
   Query Match
Best Local Similarity
Matches 9; Conserv
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US-10-660-897-11
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APPLICANT:
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APPLICANT:
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APPLICANT: Current Butles
APPLICANT: Puri, Raj K.
APPLICANT: Puri, Raj K.
APPLICANT: Puri, Raj K.
APPLICANT: Rawakami, Koji
APPLICANT: Shi, Ken J.
APPLICANT: Shi, Ken J.
APPLICANT: Joshi, Bharat H.
TITLE OF INVENTION: DELIVER CPG OLIGONUCLEOTIDES IN VIVO
FILE REFERENCE: 4239-67620
CURRENT APPLICATION NUMBER: US/10/484,991
CURRENT FILING DATE: 2004-01-26
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-29
NUMBER OF SEQ ID NOS: 96
SONTWARE PATENTION NUMBER: PCT/US02/24235
SONTWARE PATENTION NUMBER: DCT/US02/24235
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PCT-USO3-26191A-10/c

| Sequence 10, Application PC/TUS0326191A
| GENERAL INFORMATION:
| APPLICANT: OLSON, ERIC
| APPLICANT: ARAI, AKIRC
| TILL OF INVENTION: STARS - A MUSCLE-SPECIFIC ACTIN-BINDING PROTEIN
| TILL OF ILLING DATE: 2003-08-20
| CURRENT FILLING DATE: 2002-08-20
| PRIOR PILING DATE: 2002-08-20
| NUMBER OF SEQ ID NOS: 15
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 10
| LENTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND APPLICANT: HUMAN SERVICES
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          DB 1; Length 12;
                                                                         1; Indels
      Score 8.4; DB Pred. No. 23; 0; Mismatches
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                                                                                                                                                                                                                                                                                                RESULT 31
US-10-484-991-25/c
; Sequence 25, Application US/10484991
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
          0.4%;
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ORGANISM: Artificial Seguence
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Best Local Similarity 90.0
Matches 9; Conservative
             Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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LENGIH: 12
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Best Local Similarity
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
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US-10-660-897-19/C

SQUENCE 19, Application US/10660897

GENERAL INFORMATION:

APPLICANT: Jin, Cheng

APPLICANT: Chung, Mary

APPLICANT: Gladiqui-Jain, Adam

APPLICANT: Whitten, Jeffrey

APPLICANT: Whitten, Jeffrey

APPLICANT: Whitten, Jeffrey

APPLICANT: Parrell, Thomas

TITLE OF INVENTION: QUADRUPLEX FORMING NUCLEIC ACIDS AND MODULATORS THEREOF

FILE REFERENCE: 53232000800

CURRENT APPLICATION NUMBER: 1003-09-11

PRIOR PILING DATE: 2002-09-12

NUMBER OF SEQ ID NOS: 40

SOFTWARE FRANCE: FRANCE OF Windows Version 4.0

SEQ ID NO 19

LENGTH: 12
                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/10660897

| Sequence 11, Application US/10660897
| GENERAL INPORMATION:
| APPLICANT: Chung, Mary
| APPLICANT: Chung, Mary
| APPLICANT: Chung, Mary
| APPLICANT: Mitten, Jeffrey
| TITE OF INVENITON: QUARRUPER FORMING NUCLEIC ACIDS AND MODULATORS THEREOF
| TITLE OF INVENITON: QUARRUPER FORMING NUCLEIC ACIDS AND MODULATORS THEREOF
| TITLE OF INVENITON: UNMER: 105/10/60,897
| CURRENT APPLICATION NUMBER: 60/410,475
| PRIOR FILING DATE: 2002-09-11
| PRIOR FILING DATE: 2002-09-12
| NUMBER OF SEQ ID NOS: 40
| SOFTWARE: PSECSEQ for Windows Version 4.0
| SEQ ID NO 11
| LENGTH: 12
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US-10-660-897-11
; FEATURE:
; CTHER INFORMATION: quadruplex forming sequence
US-10-660-897-11
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90.0%; Pred. No. 23;
tive 0; Mismatches
                                                                                               0.4%; Score 8.4; DE 90.0%; Pred. No. 23; tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                 Query Match

Best Local Similarity 90.0

Matches 9; Conservative
                                                                                                                                                                                        1859 GAGGATGAGG 1868
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US-10-660-897-11/c
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Sequence 24, Application US/10660897

Sequence 24, Application US/10660897

GENERAL INFORMATION:

APPLICANT: Ghung, Mary

APPLICANT: Siddidui-Jain, Adam

APPLICANT: Siddidui-Jain, Adam

APPLICANT: Mitten, Jeffrey

APPLICANT: WINENTION: HIGH-THROUGHUT METHODS FOR IDENTIFYING

TITLE OF INVENTION: HIGH-THROUGHUT METHODS FOR IDENTIFYING

FILE REFERENCE: 532232000800

CURRENT APPLICATION NUMBER: US/10/660,897

CURRENT APPLICATION NUMBER: 60/410,475

PRIOR FILING DATE: 2002-09-12

NUMBER OF SEQ ID NOS: 40

SEQ ID NO 24

LENGTH: 12
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US-10-660-877-24/c
; Sequence 24, Application US/10660897
; GENERAL INFORMATION:
; APPLICANT: Jin, Cheng
; APPLICANT: Chung, Mary
; APPLICANT: Chung, Mary
; APPLICANT: Thirten, Jeffrey
; APPLICANT: Farrell, Thomas
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
; TITLE OF INVENTION: QUARRUPLEX FORMING NUCLEIC ACIDS AND MODULATORS THEREOF
; FILE REFERENCE: 532232000800
; CURRENT APPLICATION NUMBER: US/10/660,897
; CURRENT FILING DATE: 2003-09-11
; PRIOR FILING DATE: 2002-09-12
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DB 1; Length 12;
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                                                  1; Indels
Score 8.4; DB Pred. No. 23; 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 12
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  0.4%;
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APPLICANT: BARATY, DAR
APPLICANT: SHARAY, DAR
APPLICANT: SHARAY, MUHAMMAD A.
APPLICANT: LIU, TINOTHY Z.
APPLICANT: LIU, TINOTHY Z.
APPLICANT: ENWAKOV, SERGUEI
APPLICANT: CONNELL, CHARLES R.
TITLE OF INVENTION: COMPOSITIONS, METHODS, AND KITS FOR ASSEMBLING PROBES
CURRENT APPLICATION NUMBER: US/10/652,361
CURRENT APPLICATION NUMBER: US/10/652,361
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET: 3.2
SEQ ID NO 7
LENGTH: 10
                                                                                                                                                  APPLICANT: WOUDENBERG, TIMOTHY M.
APPLICANT: WOUDENBERG, TIMOTHY M.
APPLICANT: SHARAT, DAR
APPLICANT: SHARAT, DAR
APPLICANT: LIU, TIMOTHY Z.
APPLICANT: LIU, TIMOTHY Z.
APPLICANT: CONNELL, CHARLES R.
TITLE OF INVENTION: COMPOSITIONS, METHODS, AND KITS FOR ASSEMBLING PROBES TILE REFERENCE: 5049 US
CURRENT APPLICATION NUMBER: US/10/652,361
CURRENT FILING DATE: 2003-08-29
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver: 3.2
SEQ ID NO 6
LENGTH: 10
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US-10-652-361-7
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100.0%; Pred. No. 18;
tive 0; Mismatches
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                                                                                                                        Sequence 6, Application US/10652361 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
933 CCICCICI 940
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                                                                                RESULT 41
US-10-652-361-6/c
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Sequence 32, Application US/10660897

SEQUENCE 1 NFORMATION:

APPLICANT: Chang, Mary

APPLICANT: Siddiqui-dain, Adam

APPLICANT: Whiter, Jeffrey

APPLICANT: Whiter, Jeffrey

APPLICANT: Whiter D. Thomas

TITLE OF INVENTION: QUADRUPLEX FORMING NUCLEIC ACIDS AND MODULATORS THEREOF

TITLE OF INVENTION: QUADRUPLEX FORMING NUCLEIC ACIDS AND MODULATORS THEREOF

TITLE OF INVENTION: QUADRUPLEX FORMING NUCLEIC ACIDS AND MODULATORS THEREOF

TITLE OF THE REFERENCE: 532233000800

CURRENT APPLICATION NUMBER: 108/10/660,897

CURRENT FILING DATE: 2003-09-12

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PASTSEQ for Windows Version 4.0

SOFTWARE: PASTSEQ for Windows Version 4.0

LENGTH: 12
                                                                                                                                                                            Sequence 32, Application US/10660897

GENERAL INFORMATION:
APPLICANT: Jin, Cheng
APPLICANT: Jin, Cheng
APPLICANT: Siddiqui-Jain, Adam
APPLICANT: Whitten, Jeffrey
APPLICANT: Whitten, UFfrey
APPLICANT: Whitten, US/200800
TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
TITLE OF INVENTION: UNDER: US/10/660,897
CURRENT APPLICATION NUMBER: 05/410,475
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2002-09-12
NUMBER OF SEQ ID NOS: 40
SEQ ID NOS: 802
LENGTH: 12
LENGTH: 12
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RESULT 43

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RESULT 44
US-10-652-430-7
Sequence 7, Application US/10652430
Sequence 7, Application US/10652430
SEPELICANT: WOUDENBERG, TIMOTHY M.
APPLICANT: BAHRAF, UNTAWAD A.
APPLICANT: BAHRAF, UNTAWAD A.
APPLICANT: LIU, TIMOTHY Z.
APPLICANT: CONNELL, CHARLES R.
APPLICANT: HYLDIG-NIELSEN, USNS J.
TITLE OF INVENTION: MULTIPLEX DETECTION COMPOSITIONS, METHODS, AND KITS
FILE REFERENCE: 5033 US
CURRENT APPLICATION NUMBER: US/10/652,430
CURRENT PILING DATE: 2003-08-29
SOUTWARE: Patentin Ver. 3.2
SEQ ID NO 7
LENGHH: 10
TWINDER OF SEQ ID NOS: 33
SEQ ID NO 7
TENDER OF SEQ ID NOS: 33
SEQ ID NO 7
TENDER OF SEQ ID NOS: 30.
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Sequence 6, Application US/10652430

Sequence 6, Application US/10652430

GENERAL INFORMATION:
APPLICANT: WOUDGEBEG, TIMOTHY M.
APPLICANT: BAHATT, DAR
APPLICANT: BAHATT, DAR
APPLICANT: ERRARE, WUHAMAD A.
APPLICANT: ELONEL, CHARLES R.
APPLICANT: CONNELL, CHARLES R.
APPLICANT: HYLDIG-NIELERN, JERS J.
TITLE OF INVENTION: MULTIPLEX DETECTION COMPOSITIONS, METHODS, AND KITS
FILE REPREBACE: 5023 US
CURRENT APPLICATION NUMBER: US/10/652,430
CURRENT FILING DATE: 2003-08-29
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 6
LENGTH: 10
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0.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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Search completed: March 1, 2004, 15:39:30 Job time: 0.001 secs

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| GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - nucleic search, using sw model | Run on: March 1, 2004, 15:41:44; Search time 1 Seconds (without alignments) 3.916 Million cell updates/sec | Title: Perfect score: 2161 Sequence: 1 cggcccagtgatcttgaacctacactaaaattctgaagtt 2161 | Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 0.5 | Searched: 91 segs, 906 residues | Total number of hits satisfying chosen parameters: 182 | Minimum DB seq length: 8 Maximum DB seq length: 80 | Post-processing: Minimum Match 0% Maximum Match 100% Listing first 170 summaries | * | Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | SUMMARIES | * Result Query No. Score Match Length DB ID Description | 16.4 0.8 19 1 AZ788326 ACCESS | 11.4 0.5 14 1 CA798290 ACCBSS 11.4 0.5 16 1 AL696666 ACCBSS 11.1 0.5 12 1 RH169696 | 10.2 0.5 16 1 AZ788326 ACCESS 10 0.5 19 1 AZ788326 | 9.8 0.5 13 1 BQ589768 ACCESS 9.8 0.5 13 1 BH170808 ACCESS | 9.4 0.4 12 1 BG925521 ACCESS 9.4 0.4 13 1 BG926067 ACCESS | 12 9 0.4 9 1 CP307276 ACCESS | 14 9 0.4 11 CP339065 ACCESS | 9 0.4 11 1 BQ585943 ACCESS 9 0.4 11 1 BQ585943 ACCESS 9 0 4 11 1 BQ5853914 ACCESS | 9 0.4 12 1 BQ592925 ACCESS 9 0.4 12 1 BQ594497 ACCESS | 20 9 0.4 12 1 BQ595544 ACCESS | 8.8 0.4 12 1 DE59.25 ACCESS 8 0.4 12 1 DE59.25 ACCESS 8 0.4 12 1 DE59.25 ACCESS | 8.8 0.4 12 1 BQ595544 ACCESS | 8.8 0.4 12 1 CF282215 ACCESS 8.8 0.4 13 1 BQ589768 ACCESS | 8.8 0.4 13 1 BG926067 ACCESS 8.4 0.4 10 1 CF921234 ACCESS | 29 8.4 0.4 10 1 CK298980 ACCESS 30 8.4 0.4 11 1 BM395228 ACCESS | C 31 8.4 0.4 11 1 BQ590709 ACCESSION:BQ590709 C 32 8.4 0.4 11 1 BM395226 ACCESSION:BQ59226 C 33 8.4 0.4 12 1 BQ587288 ACCESSION:BQ587288 |

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Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,

Contact: Robert B. Weiss University of Utah Genome Center University of Utah

USA 308, Rm. 308 84112,

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: P column: 16
Seg primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

source

Eukarrota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Miederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

clone UUGC2M0035P16 F, genomic survey sequence

Mus musculus (house mouse)

AZ788326.1 GI:12928014

| | | linear GSS 16-FEB-200: | DEFINITION 2M0035P16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic |
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| | | AZ788326 | 2M0035P16 |
| RESULT 1 | AZ788326/c | rocus | DEFINITION |

ALIGNMENTS

GSS 16-FEB-2001

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AUTHORS
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Laboratory Mouse DNR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gill #132114 gb] kR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xillo-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA798290 14 bp mRNA linear EST 05-DEC-2002 Cac BL 611 Cac BL (Bean and Leaf from Amelonardo type Cacao) Theobroma cacao cDNA clone Cac_BL_611 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                     /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" / hote="Vector: PWD42nv; Purified genomic DWA from M. musculus C57BL/GJ (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 0.0068;
0; Mismatches 1;
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C578L/63"
                                                                                          /db_xref="taxon:10090"
/clone="UUGC2M0035P16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCCATTGTTTGTGGGAA 1004
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Best Local Similarity 94.4%;
Matches 17; Conservative (
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                                                                                                                                                           sex="Male"
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CA798290
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BH169696
BH169696.1 GI:15905071
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Best Local Similarity 85...
Best 12; Conservative
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BH169696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
                                                                         Theobroma cacao
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (basea 1 to 16) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                       Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D., Retzel, E.R. and Jones, C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Theobroma cacao"
/mol type="mRNA"
/strain="Amelonado type"
/db_xrref="taxon:1641"
/clone="Cac_BL 611"
/tissue_type="Mature leaf and mature bean"
/cell_type="Whole organ"
/lab_nost="XL-1 Blue MRF'"
/clone_lib="Cac_BL (Bean and Leaf from Amelonardo type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                3d Dundee Road, Slough, Berkshire,
Tel: 444 1664 416644
Email: Paul Jones@eu.effem.com
Seg primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                  Planta 216 (2), 255-264 (2002) 22337596
                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                  GI:26055376
                                                         Theobroma cacao (cacao)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1143 CTCCACCTATACC 1155
                                                                                                                                                                                                                                                                                                                                Contact: Jones, Paul
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Unpublished (1997)
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                                                       SOURCE
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Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image.html
Insert Length: 1662 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BH169696 12.bp DNA linear GSS 03-OCT-2001 SALK 001766 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_001766, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II, Brassicales; Brassicaceae; Arabidopsis.

| (bases 1 to 12)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Kannes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="SALK_001766"

/clone lib="Arabidopsis thaliana TDNA insertion lines"

/core ="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can
                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:2273987"

/tissue_type="well-differentiated endometrial
denocatroinomm, 7 pooled tumors"

/lab_host="DHIDB"

/clone_lib="NCI_CGAP_Utl"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 11.4; DB 1; Length 16; Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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/strain="Columbia 0"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                     Seq primer: -400P from Gibco
High quality sequence stop: 1
Location/Qualifiers
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B

Query Match Best Local

Matches

à g DEFINITION

AI696566 RESULT 5

ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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muscular C7) Muse DNR Resource (http://www.jax.org/resources/documents/duares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomicleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AR129072.1). A copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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E012680-024-020-D03-SP6 MPIZ-ADIS-024-storage root Beta vulgaris

EQS89768

BQS89768 GI:26119351

EST.
                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="B. Coli strain XL10-Gold, Tl-resistant, F-"
/clone Lib="Mouse 10kb plasmid UUGCNM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C5/BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0035 row: P column: 16
Seg primer: CGTYGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                  Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="UUGC2M0035P16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 19.
Location/Qualifiers
                      Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          956 ATCGCTACCAACGGTGGA 973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
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Best Local Similarity
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BQ589768
                                                                                                                              REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llhi.gov/bbrp/image/image.html
Insert Length: 1662 Std Error: 0.00
Seq primmer: -40UP from Gibco
High quality sequence stop: 1.

Location/Qualifiers
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//organism="Homo sapiens"
//organism="Homo:
//db xref="Laxon:9606"
//db xref="Laxon:9608"
//tissue_type="well-differentiated endometrial
//tissue_type="well-differentiated tumors"
//db host="DH108"
//db host="Organ: uferus; Vector: pCWV-SPORT6; Site_1: Sall;
//dome_therage insert size 1.75 kb. Life Technologies catalog #:
11538-014"
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(bases 1 to 16)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
  be found at http://signal.salk.edu/tdna_protocols.html"
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                                                    Score 11; DB 1; Length 12;
Pred. No. 0.5;
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AZ788326
AZ788326.1 GI:12928014
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100.0%; Pred. No. v...
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FEATURES

DEFINITION

RESULT 6 AZ788326

ACCESSION

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/clone="SALK_003378"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana thace="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 12)
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709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG925521 12 bp mRNA linear EST 06-NOV-20
HNC5-1-D3.R HNC (Human Normal Cartilage) Homo sapiens CDNA, mRNA
                                                                                                                                                                                                                     This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identification and initial characterization of 5000 expressed sequenced tags (ESTS) each from adult human normal and osteoarthritic cartilage cDNA libraries Osteoarthr. Cartil. 9 (7), 641-653 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.5%; Score 9.8; DB 1; Length 13; 44.6%; Pred. No. 5.8; 2; Indels:ve 0; Mismatches 2; Indels
               Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 558 6379
Fax: 858 558 6479
Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                              organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="Columbia 0"
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Fax: 610-270-5598
Email: sanjay kumar-1@gek.com
Seq primer: 77.
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Location/Qualifiers
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BG925521.1 GI:14320044
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                            Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 13)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes 22362189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: Not1; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Binbeck, Germany, contact: b.schulz@kws.de; cloning sites Sall-Not1, primer sites and
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Adonso,J.M., Leisse,M., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SP6-Sall-CCACGCGTCCG-5prime-cDNA-polyA-CC-Notl-T7; Note: Sequencing granted in the context of the GABI-Beet project, local Pir. Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Beta vulgaris"
/mol type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
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12472698
Contact: Weisshaar B
ADIS DNA core facility at MPIZ
ADIS DNA core facility at MPIZ
ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215082851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 13 Std Error: 0.00
Plate: 20 row: D column: 03
Plate: 20 row: D column: 03
Seq primer: SP6; CATRCGATTAGGTGACTATAG.
Location/Qualifiers
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84.6%; Pred. No. 5.8;
tive 0; Mismatches 2; Indels
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/lab_host="EMDH108"
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/clone="024-020-D03"
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HNC23-1-E8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                           Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site_1: Sal1; Site_2: Not1;
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                                                                                       1; Indels
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                                                        0.4%; Score 9.4; DB
90.9%; Pred. No. 5.4;
cive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 610-270-5598
Email: sanjay kumar-1@gsk.com
Seg primer: T7.
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                              Directional"
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es 10; Conserv
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllates; Amaranthaceae; Beta.

(aryophyllates; Amaranthaceae; Beta.

(bases 1 to 13)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

and Radelof,U.

Construction of a 'uniqene' cDNA clone set by oligomucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
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/lab_host="EMDH10B"
/clone lib="MPIZ-ADIS-024-developing root"
/clone lib="MPIZ-ADIS-024-developing root"
/clone lib="MPIZ-ADIS-05"
/clone lib="MPIZ-ADIS-05"
/clone lib="MPIZ-ADIS-05"
/clone lib="MPIZ-ADIS-05"
/clone sugar beet, lib="MpIZ-05"
/clone sugar beet, lib=
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Enthartoideae; Oryzae; Oryza.

1 (bases 1 to 9)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.L., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 13 Std Error: 0.00
Plate: 22 row: N column: 20
Seg primer: SP6; CATAQGATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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/clone="024-022-N20"
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Gaps

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Oryza sativa
Oryza sativa

Oryza sativa

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatcphyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Bhrhartoideae; Oryzeae; Oryza.

I (bases 1 to 11)

S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Wector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5. and with SstI and 3. end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"
                                                                                                                                                                                                                                                                                                                                                                           EST 18-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                             RCL1--03-K22.gl Regenerated callus lambda phage cDNA library (RCL1) Oryza sativa cDNA clone RCL1--03-K22, mRNA sequence.
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/lab_host="E.coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="Regenerated callus lambda phage cDNA library
was inserted into lambda Uni-ZAP XR vector at 5' end w:
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."
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100.0%; Pred. No. 4.8;
iive 0; Mismatches
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| cultivar="Nackdong"
| db_xref="taxon:4530"
| clone="RC11-03-7822"
| tissue_type="callus"
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CF339065.1 GI:33826512
BST.
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//oce="Vector: pBluescript SK(+); Site 1: EcoR1; Site 2: Anote="Vector: pBluescript SK(+); Site 1: EcoR1; Site 2: Anot; cBlus was treated with ABA(20um] For lhour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoR1 and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermacophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae, Oryza.

1 (bases 1 to 9)

Kim,J.S., Unn,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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//note="Vector: pBluescript SK(+); Site 1: EcoR1; Site 2: XhoI; Callus was treated with ABA(20um) for lhour. cDNA
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
                                                                                                                                                                                                                                                                                                                                                 'dev stage="proliferated callus on 2N6 media for 2 weeks"
|lab_host="E.coli SOLR"
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yorgin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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    Location/Qualifiers
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ilarity 100.0%; Pred. No. 1.1.
Conservative 0; Mismatches
                                                                                                                                                                                              /organism="Oryza sativa"
mol type="mRNN"
rulLivar="Nackdong"
/db xref="taxon:4550"
/clone="HDAl--06-D23"
/ilssue_type="callus";
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/organism="Oryza sativa"
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/clone="HDA1--06-K23"
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/cultivar="Nackdong"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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11 bp mRNA linear EST 06-DEC-2002 S015507-024-025-N20-SP6 MPIZ-ADIS-024-developing root Beta vulgaris EQNA clone 024-025-N20 5-PRIME, mRNA sequence.
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Caryophyllales, Amaranthaceae, Beta.

1 (bages 1 to 11)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligomucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                  /clone lib="MPIZ-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Not1-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                      "mol type="mRNA"
'cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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RZPD/GABI-Primary database:http://gabi.rzpd.de"
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ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
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Insert Length: 11 Std Brror: 0.00
Plate: 25 row: N column: 20
Seq primer: 8F6; CATACGATTTAGGTGACACTATAG.
Location/Qualifiers
Plate: 14 row: K column: 17
Seg primer: SP6; CATACGATTTAGGTGACACTATAG.
Location/Qualifiers
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                                                                                                 organism="Beta vulgaris"
                                                                                                                                                                                            /db_xref="GABI:186918"
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/clone="1024-014-K17"
/tissue_type="leaf"
/lab_host="EMDH108"
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/db_xref="taxon:161934"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 11)
Branig, K., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
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Bermatophyta; Magnolliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
(bases 1 to 11)
                         Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enthartoideae; Oryzeae; Oryza,
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
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                                                                                                                                                                                                                                               Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
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100.0%; Pred. No. 4.8;
tive 0; Mismatches
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/lab host="EMDHIOB"
/clone lib="MPIZ-ADIS-024-developing root"
/clone lib="MPIZ-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site 1: Sal1; Site 2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                               BQ594497 11.2 bp mRNA linear EST 06-DEC-2002 E012444-024-024-P14-SP6 MPIZ-ADIS-024-developing root Beta vulgaris cDNA clone 024-024-P14 5-PRIME, mRNA sequence.
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1 (bases 1 to 12)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., and Brungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
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SP6-Sall-CCACCGTCGG-5prime-cDNA-polyA-CC-Not1-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Pax: 00492215062851
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Insert Length: 12 Std Error: 0.00
Plate: 24 row: P column: 14
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
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Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 9; Conservative 0; Mismatches
                                                                                                                                0.4%; Score 9; DB 1;
100.0%; Pred. No. 9.7;
attive 0; Mismatches
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/note="Vector: pCMVSPORT6; Site 1: Sal1; Site 2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
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Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                       b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
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Peprantophyta, Magnoliophyta, eudicotyledons, core eudicots;
Caryophyllales, Amaranthaceae, Beta.
1 (bases 1 to 12)
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                                                                                                                                                                                                                                                                      Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung, Sequence submission managed by RZPD/GABI-Primary database: http://gabi.zzpd.de"
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/note="Vector: pCMVSPORT6; Site_1: Sall; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
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//mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
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ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Bmail: weisshaa@mpiz-koeln.mpg.de
Insert Length: 12 Std Brror: 0.00
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Seq primer: SP6; CARACGATTAGGTGACACTATAG.
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100.0%; Pred. No. 4.8;
Live 0; Mismatches
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/note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
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                                                                                        Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 12)
I (bases 1 to 12)
Meisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H., and Radelof, U.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllates; Amaranthaceae; Beta.
1 (bases 1 to 12)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
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SPG-Sall-CCAGGGTCGG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Project, Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"
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/mol type="mRNA"
/culTivar="KWS2320 (double haploid, monogerm breeding
line)"
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                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Weisshaar B
ADIS DNA core facility at MPIZ
MAx-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 12 Std Brror: 0.00
Plate: 9 row: P column: 23
Seq primer: SP6; CATACCATTTAGGGGACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-leaf"
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/clone="024-009-p23"
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       BQ587870.1 GI:26117452
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BQ592925.1 GI:26122508
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                                                                                                                                                    /clone lib="MPIZ-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saazucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-Not1, primer sites and
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8013708-024-009-P23-SP6 MPIZ-ADIS-024-leaf Beta vulgaris CDNA clone
0224-009-P23 5-PRIME, mRNA sequence.
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(aryophyllales; Amaranthaceae; Beta.

(bases 1 to 12)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., and Radelof,U., Lehrach,H.
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SP6-SalI-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7;
SP6-SalI-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7;
Sequencing granted in the context of the GABI-Bet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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/cultivar="KWS2320 (double haploid, monogerm breeding
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ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 12 Std Brror: 0.00
Plate: 22 row: A column: 12
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
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Email: weisshaagmpiz-koeln.mpg.de
Insert Length: 12 Std Brror: 0.00
Plate: 24 row: P column: 14
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
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Insert Length: 12 Std Error: 0.00
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Location/Qualifiers
                                                                                                                                                                                                                                                                                        /tissue_type="developing root"
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Pred. No. 13;
0; Mismatches
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/db xref="taxon:161934"
/clone="024-024-P14"
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|/tissue_type="developing root"
|lab_host="EmbH108"
|clone_lib="MPIZ-AbIs-024-developing root"
|/thot="Yecror: pCWVSPORT6; Site_1: Salt; Site_2: Not!;
|clone_lib=xprefire Super beet, library provided by KWS
|Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
|b.schulz@kws.de; cloning sites Sall-Not!, primer sites and
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Beta vulgaris

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 12)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,

and Radelof,U.

Beta vulgaris and value, M., Menze,A., O'Brien,J., Lehrach,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   orientation:
SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Notl-T7; Note:
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Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZFD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                  /organism="Beta vulgaris"
/wol_type="mRNA"
/culLivar="KWS2320 (double haploid, monogerm breeding
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
                                                                                                                                  ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 12 Std Brror: 0.00
Plate: 28 row: F column: 05
Seq primer: SP6; CATAGGATTTAGGTGACACTATAG.
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                                                                                                                     Contact: Weisshaar B
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BQ595544 linear EST 06-DEC-2002 E012691-024-022-A12-SP6 MPIZ-ADIS-024-developing root Beta vulgaris cDNA clone 024-022-A12 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots, Caryophyllales, Amaranthaceae; Beta.

1 (bases 1 to 12)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., and Radelof,U. Katall,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Beta vulgaris"
/mol type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Notl-T7;
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0
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ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
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schultz451-1.rst

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BQ589768 13 bp mRNA linear EST 06-DEC-2002 E012680-024-020-D03-SP6 MPIZ-ADIS-024-Storage root Beta vulgaris cDNA clone 024-020-D03 5-PRIME, mRNA sequence.
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HNC23-1-E8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
                                                                                                                                                                                                                                                                                                                    Beta vilgaris

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

(bases 1 to 13)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J: 32 (5), 845-857 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KW82320 (double haploid, monogerm breeding
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Pred. No. 23;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
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Insert Length: 13 Std Brror: 0.00
Plate: 20 row: D column: 03
Seq primer: SF6; CATACGATTRAGTGGCACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:161934"
/clone="024-020-D03"
/tissue_type="storage_root"
/lab_host="EMDH10B"
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Matches 10; Conserv
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                                                                                                RESULT 26
BQ589768/c
                                                                                                                                                                        DEFINITION
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PUBMED
COMMENT
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                       Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
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14ETL--09-K01.bl Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--09-K01, mRNA sequence.
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0
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 12)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Xim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Torgin, KyeongJi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355
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               | db xref="GABI:191314" | db xref="GABI:191314" | db xref="taxon:161934" | db xref="taxon:161934" | dclone="1024-022-A12" | lab lost="SMDH10B" | lab lost="EMDH10B" | lab lost="EMDH10B" | lab lost="Wector: pCMVSPORT6; Site 1: Sall; Site 2: Not1; ODNA library from sugar beet, library provided by KWS | Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa"
/organism="Oryza sativa"
/uoltivar="Nackoon;"
/db xref="taxon:4530"
/clone="14ETL--09-K01"
/tissue_"Yppe="lagaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF282215.1 GI:33659602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ilarity 83.3%;
Conservative
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Oryza sativa
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CF282215
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sequence. BG926067

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organism="Glycine max"
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Nicotiana benthamiana
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COMMENT
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                    1 (bases 1 to 13)
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 10)
Scheffler, B.E., Huang, S., Liu, X., Nguyen, H., Duke, M. and Stacey, G.
Expressed sequence tags from soybean root hair subtractive cDNA
                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                       GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
                                                                                                                                                                           Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and costeoarthritic cartilage CDNA libraries osteoarthr. Cartil. 9 (7), 641-653 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Contact: Gary Stacey
University of Missouri
UN Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-4752
Fax: 573-882-0588
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83.3%; Pred. No. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                          Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay kumar-1@gsk.com
Seg primer: T7.
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Single pass sequence
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CF921234.1 GI:38192028
 GI:14320590
                                                                                                                                                                                                                                                                                     Contact: Sanjay Kumar
UW2109
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                                     Homo sapiens (human)
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                                                      Homo sapiens
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Matches 10; Conserv
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3G926067.1
                                                                                                                                                              Lark, M.W.
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CF921234/c
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/done="nBMDJ48"
/ilssue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"

/lab host="DH10B-TonA"
/lab host="DH10B-TonA"
/lone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCWVSport6.1; Site 1: ECORI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.

1 (Dases 1 to 10)

Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST761633
Conteat: Romanic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-arrayatigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: GTA ATA GGA CTC ACT ATA GGG C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Losober 10 bp mRNA linear EST 15-DEC-2003
EST751694 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NBMDJ48 3'
CK298980
                                                                                                                                                                                          CDNA clones
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                                                                                             /tissue_type="root hairs"
/clone_lib="Soybean root hair subtracted cDNA library
                                                                                                                                                                                    /note="Organ: root hairs; Vector: pCR2-1 Topo; cDNA ogenerated from soybean root hair tissue treated with Bradyrhizobium japonicum for 3 hours."
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llarity 90.0%; Pred. No. 5.3;
Conservative 0; Mismatches 1; Indels

    .10
    /organism="Nicotiana benthamiana"

/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
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/db_xref="taxon:4100"
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orientation:
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Best Local Similarity
Matches 9; Conserv
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BM395226/c
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                                                                                                                             BM395228 17-JAN-2002 50072-2-8-B05.r.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence.
                                                                                                                                                                                                                                                         Tetrahymena thermophila

Eukaryota, Alveolata; Ciliophora; Oligohymenophorea;

Hymenostomatida; Tetrahymenina; Tetrahymena.

Hymenostomatida; Tetrahymenina; Tetrahymena.

E [ bases 1 to 11)

S Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,

Frankel,J. and Klobutcher,L.

FST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllaies; Amaranthaceae; Beta
1 (Dases 1 to 11)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
and Radelof,U.
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/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: T3.
Location/Qualifiers
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Best Local Similarity 90.0%;
Matches 9; Conservative
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12472698
Contact: Weisshaar B
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1973
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1964 AGTTTTTTT
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BM395228/c
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/tissue type="storage root"
/lab_host="RMDH10B"
/clone lib="MPIZ-ADIS-024-storage root"
/note="Vector: pcMVSPORT6; Site_1: Sall; Site_2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-Not1, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BM395226
50072-2-8-B04.f.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
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Turkwhiz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkwhiz AP
Molecular Genetics and Cell Biology
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/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA" /colltivar="KWS2320 (double haploid, monogerm breeding
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Tetrahymena thermophila
Eukaryota, Alveolata, Ciliophora, Oligohymenophorea,
Hymenostomatida, Tetrahymenina, Tetrahymena.
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llarity 90.0%; Pred. No. 11;
Conservative 0; Mismatches 1; Indels
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 11 Std Error: 0.00
Plate: 18 row: 0 column: 24
Seq primer: SP6; CATACGATTAAGGTGAACACTATAG.
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/mol_type="mRNA"
/strain="CU428.1"
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920 E. 58th Street, Chicago, IL 60637,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: apturkew@midway.uchicago.edu
Seq primer: T3.
                                                                                                                                                                                                                                                                                                                     'organism="Beta vulgaris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:161934"
/clone="024-018-024"
                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="GABI:189410"
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BQ587706 12 bp mRNA linear EST 06-DEC-2002 E012340-024-010-G19-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone 024-010-G19 5-PRIME, mRNA sequence.
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                                       RESULT 34
BQ587706/c
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BQ589761
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KEYWORDS
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//clone lib="WPIZ-ADIS-024-leaf" |
//note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: Notl;
conA library from sugar bett, library provided by KWS
Kleinwanziebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-Notl, primer sites and
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E012246w-024-010-G19-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA
clone 024-010-G19 5-PRIME, mRNA sequence.
BQ587288 1 GI:26116870
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1 (bases 1 to 12)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., and Radelof,U.

2018 Farmingowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "mol type="mRNA"
cultivar="KWS2320 (double haploid, monogerm breeding
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Prof. Christian Jung; Sequence submission mana
RZPD/GABI-Primary database:http://gabi.rzpd.de"
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                                                           0.4%; Score 8.4; DB 1; Length 11; 90.0%; Pred. No. 11; lve 0; Mismatches 1; Indels
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Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
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Insert Length: 12 Std Error: 0.00
Plate: 10 row: 6 column: 19
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
Location/Qualifiers
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tive 0; Mismatches
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/organism="Beta vulgaris"
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/db xref="taxon:161934"
/clone="024-010-G19"
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'lab_host="EMDH10B"
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E012680-024-020-P03-SP6 MPIZ-ADIS-024-Storage root Beta vulgaris CDNA clone 024-020-P03 5-PRIME, mRNA sequence.
BQS89761.1 GI:26119344
EST.
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/olone_lib="MPIZ-ADIS-024-leaf"
/note="Vector: pcMvSPORT6; Site_l: Sall; Site_2: Notl;
CDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Binbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-Notl, primer sites and
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Beta vulgaris
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; endicots;
Caryophylalas; Amaranthaceae; Beta.
1 (bases 1 to 12)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
and Radelof,U., Dehracon, Merze,A., O'Brien,J., Lehrach,H.
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SP6-SalI-CCACGCGTCCG-Sprime-cDNA-PolyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local Pi: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"
                                                                                                                                                                                                                                   Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
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                                                                                                                                                                                                                                                                                                                                                                                      Contact: Weisshaar B
ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
CAX-DON-Linne Weg 10, 50829 Koeln, Germany
FAX: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 10 row: G column: 19
Seq primer: SP6, CATACGATTAGGTGACACTATAG.
Location/Qualifiers
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/db_xref="taxon:161934"
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KEYWORDS
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808 TGTAAGAAA 817

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12 TGGAAGAAA 3

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AQU50979 12 bp DNA linear GSS 24-MAR-1999 nbxb0004dDllr CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nbxb0004H22r, genomic survey
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/note="Vector: pCMVSPORT6; Site_l: Sal1; Site_2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Binbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplandes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Beta vulgaris"
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/cultivar="KWS2320 (double haploid, monogerm breeding
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                                                                                                                                           Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 17 row: P column: 07
Seg primer: SP6; CATACGATTAGGTGACACTATAG.
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Tel: 864 656 7288
Fax: 864 656 4293
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Clemson University
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/lab_host="EMDH108"
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Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
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                                                                                                                     PUBMED
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 12)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
and Radelof,U.
                                                                                                                                                                                                           Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Herwig, R., Schulz, B., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U. Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                       Beta vulgaris
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales, Amaranthaceae, Beta.
1 (bases 1 to 12)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing granted in the context of the GABI-Beet project, Local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung, Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="caxon:161934"
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/clone="024-020-P03"
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/clone lib="MPIZ-ADIS-024-storage root"
/note="Vector: pGWNSPORTE; site 1: Sall; Site 2: Not!;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQS91624 117-P07-SP6 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-017-P07 5-PRIME, mRNA sequence.
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Weisshaar B
ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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Insert Length: 12 Std Brror: 0.00
Plate: 20 row: P column: 03
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
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/organism="Trypanosoma brucei rhodesiense"
/wol type="genomic DNA"
/wub species="rhodesiense"
/wub species="rhodesiense"
/db xref="teaxon:31286"
/dow_stage="Bloodstream form"
/clone|lib="WMVAT4 shearst genomic library"
/clone|lib="WMVAT4 shearst genomic library"
/note="Vector: pCR-Script Amp SK(+) (Stratagene); Site_1:
Srf i; Genomic DNA was isolated from a cloned population
of bloodstream trypanosomes reexpressing the MVAT4
metacyclic variant surface glycoprotein (VSG). For the
shotgun library construction, the DNA was mechanically
sheared to give a tight size distribution, then
blunt-ended with T4 DNA polymerase. Following
dephosphorylation with Shrimp Alkaline Phosphatase, DNA
fragments were cloned into the pCR-Script vector
(Stratagene)."
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RCL1--03-M05.gl Regenerated callus lambda phage cDNA library (RCL1) Oryza gativa cDNA clone RCL1--03-M05, mRNA sequence.
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1 (Dases 1 to 8)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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/clone="RCL1--03-M05"
/tissue_type="callus"
/drssue_type="callus"
/lab_host="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Nackdong"
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Best Local Similarity 90.0.
Lie 9; Conservative
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                                                                                                                                                                                                                            /cione="noxioustair"
/tissue_type="Leaf"
/lab_host="Eaf"
/lab_host="Eaf"
/lab_host="Eaf"
/clone lib="Cudi Rice BAC Library"
/clone lib="Cudi Rice BAC Library"
/note="Vector: pBeloBAC11; Site 1: HindIII; Site 2:
HindIII; Rice is one of two most popular grains in the
world Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledonous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 431 Mbp
(Arumuganathan and Earle, 1991). The relatively small
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies. In
order to facilitate positional cloning, physical mapping
and genome sequencing of rice, we have constructed a BAC
library from Oryza sativa, Nipponbare variety. The
library contains 36 864 clones with an average insert size
of 128.5 Kb providing 10.9 haploid genome equivalents. The
deep coverage allows the isolation a particular sequence
with a probability of 99.9 %. Two high density filters,
each containing 18, 432 clones (doubly spotted), represent
the whole library for colony screening."
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A survey of the Trypanosoma brucei rhodesiense genome using shotgun sequencing
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John Donelson's Laboratory
Howard Hughes Medil Institute
300 EMRB, Dept. of Biochemistry, University of Iowa, Iowa City, IA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                              /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/strain="Japonica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trypanosoma brucei rhodesiense
Trypanosoma brucei rhodesiense
Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
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97237559
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Insert Length: 700 Std Error: 200
Seg primer: T3 primer
Class: shotgun.
                                                                                                                                                         /cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="nbxb0004H22r"
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     ity sequence stop: 1
Location/Qualifiers
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Fax: 319 335 6764
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Matches 9; Conserv
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7LEAF--08-M07.gl Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--08-M07, mRNA sequence.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.

1 (bases 1 to 8)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeongji, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                            Contact: Nahm B.H.
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
Genomics and Bloinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@pio.myongji.ac.kr.
Location/Qualifiers
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100.0%; Pred. No. 1.3e+02;
rative 0; Mismatches 0; Indels
Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
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14ETL--03-L19.gl Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--03-L19, mRNA sequence.
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Divaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta, Spermatophyta; Viridiplantae, Streptophyta; Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales; Poaceae,

Ehrhartoideae, Oryzeae, Oryza,

1 (bases 1 to 8)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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REFERENCE AUTHORS

RESULT 43 CF312818/c DEFINITION

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CF312817
ABF--08-L15.b1 ABF3-overexpressing transgenic rice plasmid cDNA
Library (ABF) Oryza sativa cDNA clone ABF--08-L15, mRNA sequence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 9)
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Large-scale Sequencing Analysis of Rice ESTs
Umpublished (2003)
Contact: Nahm B. H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Ehrhartoideae; Oryzeae; Oryza.

1 (Dases 1 to 9)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pGR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
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/tissue type="leaf"
/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone lib="ABF3-0-cexpressing transgenic rice plasmid con a library (ABF)"
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                                                                                                                                                                                                                               Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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0.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.'No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indele
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/cultivar="Nackdong"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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CF312817.1 GI:33684578
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JOURNAL
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CF312817
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9 bp mRNA linear EST 15-AUG-2003 ABF--03-C20.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--03-C20, mRNA sequence.
                                                                                                                                                                                                                                                                                    CF312818

ABF--08-L15.gl ABF3-overexpressing transgenic rice plasmid cDNA
llibrary (ABF) Oryza sativa cDNA clone ABF--08-L15, mRNA sequence.
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Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
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1. (bases 1 to 8)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, Y.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University Yorghin, Kyeongqi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db xref="taxxon:4530"
/clone="ABF--08-L15"
/tissue type="leaf"
/dev_stage="14 days after germination"
/lab_host="s.coli DH:08"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.4%; Score 8; DB 1; Length 8;
100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0; Indele
                                                          0; Indels
       Query Match 0.4%; Score 8; DB 1; Length 8; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 8; Conservative 0; Mismatches 0; Indele
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/mol_type="mRNA"
/cultivar="Nackdong"
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                                                                                                               1966 TTTTTTT 1973
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Matches 8; Conserv
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CF309109/c
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ACCESSION

LOCUS

à Db

0

Gaps

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/organism="Oryza sativa"

/mol type="mRNA"

/mol type="mRNA"

/mol type="mRNA"

/db xref="taxon.4530"

/db xref="taxon.4530"

/clone="NACL--06-H06"

/tissue type="callus"

/dev stage="proliferated callus on 2N6 media for 30 days"

/lab host="E.coli DH108"

/lab host="E.coli DH108"

/lone lib="Rice callus plasmid cDNA library (NACL)"

/note="Tector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
9 bp mRNA linear BST 18-AUG-2003 NACL--06-H06.bl Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--06-H06, mRNA sequence.
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Oryza sativa
Oryza sativa
Oryza sativa
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzae; Oryza.

1 (bases 1 to 10)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Isng,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                  Oryza sativa

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Brhartoideae; Oryzeae; Oryza.

1 (bases 1 to 9)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Xim,Y.-K. and Nahm,B.H.

Jarge-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Nahm B.H.

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc., Division
Genomics and Bloinformatics, MyongJi University
Yorgin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@pio.myongJi.ac.kr.

Location/Qualifiers
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JMT--02-J09.g1 AtJMT-overexpressing transgenic rice plasmid CDNA
library (JMT) Oryza sativa CDNA clone JMT--02-J09, mRNA sequence.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhrahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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0.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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AUTHORS
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                                                                                                                ACCESSION
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E 1 (Dases 1 to 9)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJin, Kyeonggi, Korea
Tel: 82 31 330 6193

Fax: 82 31 321 6355
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| dev_stage="proliferated callus on 2N6 media for 2 weeks"
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| /clone lih="scoll DH108"
| /clone lih="collAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
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HD--09-A13.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--09-A13, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                            0;
                      /dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
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Location/Qualifiers
1. .9
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                                                                                                                                                                                                                                                                                                    0.4%; Score 8; DB 1; Length 9;
100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0; Indels
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/cultivar="Nackdong"
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Best Local Similarity
Matches 8; Conserva
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Oryza sativa
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DEFINITION

RESULT 46 CF318771

ð 엄 ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

TITLE JOURNAL

COMMENT

REFERENCE AUTHORS source

FEATURES

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Gaps .. 0 EST 18-AUG-2003

FEATURES

RESULT 47 CF330649

21

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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Shrhatrodeae; Oryzaa.

Enthatrodeae; Oryzaa.

Extim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggblo.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                           CF322692
HDN--01-M19.gl OBHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--01-M19, mRNA
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HNC5-1-D3.R HNC (Human Normal Cartilage) Homo sapiens CDNA, mENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="HDN--01-M19"
/tissue type="callus"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 12)
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100.0%; Pred. No. 20;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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                                                                                                                                                                                                                               CF322692.1 GI:33793616
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183 GGAAGCCC 190
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Oryza sativa
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Best Local Similarity
Matches 8; Conserv
                                    8 GGAAGCCC
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BG925521/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CA794390 10 bp mRNA linear EST 05-DEC-2002 Cac_BL_1340 Cac_BL (Bean and Leaf from Amelonardo type Cacao)
Theobroma cacao cDNA clone Cac_BL_1340 5', mRNA sequence.
                                                                                                                                                                                                            /note="Vector: pCR4-TOPO; Site_1: BcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Malvales, Malvaceae, Byttnerioideae,
                                                                                                                                                                          /clone lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene discovery and microarray analysis of cacao (Theobroma cacao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
Retzel,E.R. and Jones,C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBK-CMV; Bean and leaf tissue from Amelonado type Cacao tree."
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                                                                                                                                   /dev stage="14 days after germination"
/lab_host="E.coli DH10B"
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100.0%; Pred. No. 9.5;
tive 0; Mismatches
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Email: Paul.Jones@eu.effem.com
Seq primer: T3.
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                  /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
                                                                           /db xref="taxon:4530"
/clone="JMT--02-J09"
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Planta 216 (2), 255-264 (2002)
22337596
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                                                                                                                   /tissue_type="leaf"
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Beta vulgaris
Beta vulgaris
Beta vulgaris
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 12)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
and Radelof,U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 06-DEC-2002
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                                                                                                                                                      GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
719 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
711 610-270-7245
Fax: 610-270-5598
Email: sanjay kumar-1@gsk.com
Seq primer: T7
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/cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQS87288 12 bp mRNA linear EST 06-DEC.
E012340w-024-010-G19-SP6 MPIZ-ADIS-024-leaf Beta vulgaris CDNA
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                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="raxon:8606"
/tiseue_type="cartilage"
/lab host="E.coli DH10 B"
/clone lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site_1: Sal1; Site_2: NotI;
Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries Osteoarthr. Cartil. 9 (7), 641-653 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Weisshaar B
ADIS DNA core facility at MPIZ
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 10 row: G column: 19
Seg primer: SP6; CATACGATTAAGGTGACTATAG.
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.36;
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Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches
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Pred. No.
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BQ587288.1 GI:26116870
                                                                                                                      Contact: Sanjay Kumar
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VERSION
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BQ587288
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BQS87706
B012240-024-010-G19-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
024-010-G19 5-FRIME, mRNA sequence.
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 12)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
                                                                         /lab host="EMDHIOB"
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/note="Vector: pGWVSPORT6; Site_1: SalI; Site_2: NotI;
CDNA_library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                          SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Not1-T7; Note: Sequencing granted in the context of the GABI-Beet project, local Pi: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"
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/cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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ADIS DNA core facility at WPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 12;
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Insert Length: 12 Std Brror: 0.00
Plate: 10 row: G column: 19
Seg primer: SP6; CATACGATTTAGGTGACTATAG.
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100.0%; Pred. No. 36;
ive 0; Mismatches
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/organism="Beta vulgaris"
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LOCUS

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BG927896 11 bp mRNA linear EST 06-NOV-2001
HNC45-1-D11.R HNC (Human Normal Cartilage) Homo sapiens CDNA, mRNA
                                                                                                                                                             EST 06-NOV-2001
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Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 11)
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
                                                                                                                                                           BG927412 1.00 11 bp mRNA linear BST 06-NOV-200 HNC1-1-G11.R HNC (Human Normal Cartilage) Homo sapiens CDNA, mRNA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lark,M.W.

Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries
Osteoarthr. Cartil. 9 (7), 641-653 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="cartilage"
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birectional"
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11.8%; Pred. No. 26;
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 610-270-5598
Email: sanjay_kumar-1@gsk.com
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BG927412.1 GI:14321935
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Best Local Similarity
    50 GAGAATTC
                                              1 GAGAATTC
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                                                                                                                   RESULT 55
BG927412
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AUTHORS
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KEYWORDS
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BQ595423
BQ595423.1 GI:26125006
EST.
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/clone lib="MPIZ-ADIS-024-developing root"
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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
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SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local P1: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Notl-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"
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                                                                                                                                            Query Match 0.4%; Score 8; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 36; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 00492215062851
Email: weisshaa@mpiz-koein.mpg.de
Insert Length: 13 Std Error: 0.00
Plate: 22 row: N column: 20
Seq primer: SP6; CATACGATTTAGGTGACATATAG.
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|clone="024-022-N20"
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BQ595423
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11 bp mRNA linear EST 06-DEC-2002 E012531-024-014-K17-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone BQ585943
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Gore eudicots;
Caryophylales; Magnoliophyta; eudicotyledons; core eudicots;
Caryophylales; Amaranthaceae; Beta.
1 (bases 1 to 11)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
and Radelof,U.
and Radelof,U.
Construction of a 'unigene' CDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
                                                                                                                            BM395997
5009-0-15-D12.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:5911"
/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/clone lib="Chilcoat/Turkewitz SK+; Details on library
prote="vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 11)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
Frankel, J., and Kributcher, L.
Erankel, J., and Kributcher, L.
Erankel, J., and Kributcher, L.
Erankel, T.
Erankel, T.
Erankel, T.
Erankel, T.
Erankel, Growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago, 16 60637, USA
Fra: 773 702 4317
Frax: 773 702 4317
Email: apturkew@midway.uchicago.edu
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Bukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena
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Pred. No. 26;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Tetrahymena thermophila"
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/strain="CU428.1"
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ADIS DNA core facility at MPIZ
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Location/Qualifiers
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Matches 9; Conservative (
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/db_xref="taxon:591"
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/note="Vector: BlueScriptz SK*, betails on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
                                                                                                                         GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Fax: 610-270-5598
Fax: 610-270-5598
Seq primer: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tetrahymena thermophila
Tetrahymena thermophila
Bukaryoca, Alveolata; Ciliophora; Oligohymenophorea;
Bukaryoca, Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.

1 (bases 1 to 11)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
BST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
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/lab host="E.coli DH10 B"
/note="Type="tothuman Normal Cartilage"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Turkewitz AP Molecular Genetics and Cell Biology Molecular Genetics and Cell Biology University of Chicago University of Chicago, IL 60637, USA Tel: 773 702 4374.

Email: apturkew@midway.uchicago.edu
osteoarthritic cartilage cDNA libraries Osteoarthr. Cartil. 9 (7), 641-653 (2001) 21482651 [11597177] Contact: Sanjay Kumar
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Pred. No. 26;
0; Mismatches
                                                                                                                                                                                                                                                                                                           l. .11
/organism≂"Homo sapiens"
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Gaps

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/clone="Ds01_0le11"
/tissue_Yppe="leaf"
/tissue_Yppe="leaf"
/dv stage="1-nonth seedlings - 1 cm tall - 8 leaf"
/dv stage="1-nonth seedlings - 1 cm tall - 8 leaf"
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/clone="024-025-N20"
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/note="rector: pcwvsport6; Site 1: Sal1; Site 2: Not1;
/note="rector: pcwvsport6; Site 2: Not1;
/note: pcwvsport
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
rosida; eurosida II; Brassicales; Brassicaceae; Descriania.

1 (bases 1 to 11)

2 (bases 1 to 11)

3 (bases 1 to 11)

3 (bases 1 to 11)

3 (bases 1 to 11)

4 (bases 1 to
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SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Ratharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Bastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KlA
mol type="mRNA"
cultivar="KWS2320 (double haploid, monogerm breeding
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/db_xref="taxon:89411"
                                                                                                                              db_xref="GABI:192937"
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Location/Qualifiers
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Tel: (613) 759-1662
Fax: (613) 759-1701
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Matches 9; Conservative
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1 (bases 1 to 11)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Glore lib="MPIZ-ADIS-024-leaf"
/Glore="Vector: pCMVSPORT6; Site 1: Sall; Site 2: Not1;
/note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: Not1;
Soll library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-Not1, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-Not1-T7; Note:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung: Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/cultivar="KW82320 (double haploid, monogerm breeding
line)"
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ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
MAX-Planck-Institute for Plant Breeding Research
Fax: 00492215062851
Email: weisshaa@mpiz.koeln.mpg.de
Insert Length: Il Std Error: 0.00
Plate: 25 row: N column: 20
Seg primer: SP6; CATACGATTAGGGGACCTATAG.
              Max-Planck-Institute for Plant Breeding Research
                                               Carl von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: welsshaa@mpiz_koeln.mpg.de
                                                                                                                                                                                  Insert Length: 11 Std Brror: 0.00
Plate: 14 row: K column: 17
Seg primer: SP6; CATACGATTTAGGTGACACTATAG.
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/clone="024~014-K17"
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/lab_host="EMDH10B"
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DEFINITION

RESULT 62

d à

CF323154

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

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12 bp mRNA linear EST 06-DEC-2002
8013708-024-009-P23-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
BQ587870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="MPIZ-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site 1: Sal1; Site 2: Not1;
/note="Vector: pCMVSPORT6; Site 1: Sal1; Site 2: Not1;
SolDA library from sugar beet, library, provided by KWS
Kleinwanzlebener Saatzucht AS Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 12)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., and Radelof,U., Ethrach,H.
                                     Caryophyllales, Amaranthaceae, Beta.

1 (Dases I to 11)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,

Brungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

and Radelof,U.

construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J 32 (5), 845-857 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Beta vulgaris"
|mol_type="mRNA"
|cultivar="KWS2320 (double haploid, monogerm breeding
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                              Contact: Weisshaar B
ADIS DNA core facility at MPIZ
ADIS DNA core facility at MPIZ
MAx-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 049221506281
Fmail: weissha@mpiz-koeln.mpg.de
Insert Length: 11 Std Brror: 0.00
Plate: 30 row: P column: 02
Seq primer: SP6.
Location/Qualifiers
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Pred. No. 26;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:161934"
/clone="024-030-P02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="GABI:936732"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'tissue_type="leaf"
'lab_host="EMDH10B"
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Similarity 81.8%;
9; Conservative (
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Matches 9; Conserv
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                                                                 REFERENCE
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Beta vulgaris
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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/clone="HDN--03-B04"
/tissue type="callus"
/dev stage="prolifered callus on 2N6 media for 2 weeks"
/lab host="E.05HDRCL-overexpressing transgenic rice lambda phage cDNA library II (HDN)"
                                                                                                                                                                                                                                                                                                             HDN--03-B04.gl OsHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--03-B04, mRNA
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (Mases 1 to 11)
Song's I. V. Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,
Song, S. I., Kim, J. K., Kim, Y. K. and Nahm, B. H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B. H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Toglin, Kyeongqi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Increasive form rice Historic Tamba Unitar Site 1: EcoRI; Site 2: Xhol; CDNA was inserted into lambda Unitar XPR vector at S, end with EcoRI and 3' end with Xhol site. mRNA was derived from rice Histore Deacetylase overexpression
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Location/Qualifiers
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                                                                      2; Indels
                         1;
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81.8%; Pred. No. 26;
cive 0; Mismatches
                      ВВ
                      Score 7.8; DB Pred. No. 26; 0; Mismatches
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/mol_type="mRNA"
/cultivar="Nackdong"
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                         0.4%;
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                                                                                                                    371 AGAGAGATAGT 381
                                                                                                                                                                 1 AGAGAACTAGT 11
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Oryza sativa
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source

FEATURES

RESULT 63 CF543031/c

Matches

LOCUS

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

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Gaps

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db xref="GABI:190373"

/db xref="taxon:161934"

/dlone="1024-020-P03"

/clone="1024-020-P03"

/tissue_type="storage root"

/lab host="EMDH10B"

/clone lib="MPIZ-ADI5-024-storage root"

/note="Yector: pCWYSPORT6; Site_1: Sall; Site_2: Notl;

CDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:

b. schulz@kws.de; cloning sites Sall-Notl, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma.
1 (bases 1 to 12)
Bl-Sayed, N.M.A. and Donelson, J.E.
A survey of the Trypanosoma brucei rhodesiense genome using shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B07312 G360T3 MVAT4 sheared genomic library Trypanosoma brucei rhodesiense genomic clone G360, genomic survey sequence.
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Contact: El-Sayed NWA
John Donelson's Laboratory
Howard Hughes Medical Institute
300 EMRB, Dept. of Biochemistry, University of Iowa, Iowa City, IA
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/clone_lib="MVAT4 sheared genomic_library"
/note="Vector: pCR-Script Amp_SK(+) (Stratagene); Site_l:
                                                                                                                                                                                                                                                                                                                                                                                                           Note:
                                                                                                                                                                                                                                                                                                                                                                                                    SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Notl-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                        /mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
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Trypanosoma brucei rhodesiense
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.4%; Score 7.8; DB 1; Length 12; llarity 81.8%; Pred. No. 45; Conservative 0; Mismatches 2; Indels
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Fax: 319 335 6764
Email: nelsayed@vaxa.weeg.uiowa.edu
Insert Length: 700 Std Error: 200.00
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/sub_species="rhodesiense"
/db_xref="taxon:31286"
                                  l. .12
/organism="Beta vulgaris"
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Class: shotgun.
Location/Qualifiers
Location/Qualifiers
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E012680-024-020-P03-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-020-P03 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, Caryophyllales, Amaranthaceae; Beta.

(aryophyllales, Amaranthaceae; Beta.
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., and Radelof,U., Eahl,D., Wruck,W., Menze,A., C'Brien,J., Lehrach,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Not1-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schmeider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="leaf"
/lab_host="EMDH10B"
/clone lib="MPIZ-ADIS-024-leaf"
/note="Vector: powVSPORT6; Site 1: Sall; Site 2: Notl;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                                                                                                                                                                                                                                                                            1. .12
/organism="Beta vulgaris"
/mol type="mRNA"
/culTivar="KW82320 (double haploid, monogerm breeding
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
                                Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Ilnsert Length: 12, Std Error: 0.00
Plate: 9 row: P column: 23
Seq primer: SP6; CATAGGATTTAGGATGACACTATAG.
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Email: weisehaa@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 20 row: P column: 03
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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|db xref="taxon:161934"
|clone="024-009-P23"
                                                                                                                                                                                                                                                   Location/Qualifiers
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BQ589761.1 GI:26119344
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Beta vulgaris
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Matches 9; Conserva
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Direct Submission

Direct Submission

Direct Submission

Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage,

z rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (B-mail:

seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces ervazzii, Zygosaccharomyces rouxii,

Saccharomyces Kluyverii, Kluyveromyces thermotolerans, Kluyveromyces saccharomyces hansenii and var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CUNSUBESN
13 end of clone AR0AA018H04 of library AR0AA from strain CBS 732 of Zygosaccharomyces rouxii, genomic survey sequence.
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                                                                                                                                                        DNA
I; Genomic DNA was isolated from a cloned population
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Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bon,E., Bror,E., Bror,E., Exciter,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
                   of bloodstream trypanosomes reexpressing the MVAT4 metacyclic variant surface glycoprotein (VSG). For the shotgun library construction, the DNA was mechanically sheared to give a tight size distribution, then blunt-ended with T4 DNA polymerase. Following dephosphorylation with Shrimp Alkaline Phosphatase, DNA fragments were cloned into the pCR-Script vector
                                                                                                                                                                                                                                                                                                                       Gaps
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de Montigny, J., Straub, M., Potier, S., Tekaia, F., Dujon, B.,
Wincker, P., Artiguenave, F. and Souciet, J.
Genomic exploration of the hemiascomycetous yeasts: 8.
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Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces
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                                                                                                                                                                                                                                                               Score 7.8; DB 1; Length 12; Pred. No. 45;
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/mol_type="genomic DNA"
/strain="CBS 732"
                                                                                                                                                                                                                                                                                                                       0; Mismatches
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FEBS Lett. 487 (1), 52-55 (2000)
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CNS06E5N/c
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CF307431

HDA1--06-K23.gl OsHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDA1) Oryza sativa cDNA clone HDA1--06-K23, mENA
                                                                                                                                                                                                                                         CF307276

9 bp mRNA linear BST 15-AUG-2003 HDA1--06-D23.gl OsHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDA1) Oryza sativa cDNA clone HDA1--06-D23, mRNA
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                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 9)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University Trogin, KyongGi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355
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                                                  Score 7.6; DB 1; Length 9;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa"

/mol type="mRNA"

/oultivar="Nackdong"

/db xref="taxon:4550"

/clone="HDA1--06-D23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="callus"
/clone="AR0AA018H04"
/clone_lib="AR0AA"
/note="end : T3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                            CF307276.1 GI:33679037
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                                                                0.4%;
ilarity 87.5%;
Conservative
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Best Local Similarity
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CF307276/c
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KEYWORDS
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CF313414

HD--01-I15.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-I15, mRNA sequence.
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/dev stage="proliferated callus on 2N6 media for 2 weeks"
/dab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                   /dev stage="Seedlings"
/clone lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 9)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scalle Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="vector: pCR4-TOPO; Site 1: ECORI; Callus was treated with ABA(20um) for lhr. Oligo-capped mRNA was reverse transcribed and then used for PCR: mRNA was derived from rice Histone Deacetylase overexpression line."
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                                                                                                                                                                                                                                                                                                              Length 9;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                           Query Match 0.3%; Score 7.4; DB 1; Length 9; Best Local Similarity 88.9%; Pred. No. 1.1e+02; Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
                                               'organism="Glycine max"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4530"
/clone="HD--01-115"
                                                                                                                  /db_xref="taxon:3847"
/clone="D06G10"
                                                                                                                                                                    tissue type="Roots"
Location/Qualifiers
                                                                   /mol_type="mRNA"
/cultivar="Peking"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="OsHDAC
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CF313414
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KEYWORDS
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Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D06G10 G10 14.abl cDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone D06G10 5', mRNA sequence.
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0
                                  Oryza sativa
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Voryza; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzaee; Oryza.

1 (bases 1 to 9)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="HDA1--06-K23"
/tissue_type="callus"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone lib="OstbAc1-overexpressing transgenic rice lambda
phage cDNA library I (HDA1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fincte="Vector: pBiuescript SK(+); Site_1: Bookl; Site_2: Arboi; Callus was treated with ABAA(30um) for Ihour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with Ecokl and 3' end with XhoI site. mRNA was derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                  Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Pred. No. 1.1e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Oryza sativa"
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Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:4530"
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/cultivar="Nackdong"
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  CF307431.1 GI:33679192
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CA850813
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  VERSION
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Gaps

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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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88.9%; Pred. No. 1.1e+02;
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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S Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Enrhartoideae; Oryzeae; Oryzea.

I (base 1 to 9)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.L., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CF323490 9 bp mRNA linear EST 18-AUG-2003 HDN--03-P21.gl OsHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--03-P21, mRNA
                                                   CF313414

9 bp mRNA linear EST 15-AUG-2003

HD--01-115.bl OsHDACl-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-115, mRNA sequence.
                                                                                                                                                                                                                                                                                    Oryza sativa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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CF323490
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RESULT 72
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XDOI; DDNA was inserted into lambda Uni_ZAP XR vector at XDOI; DNA was inserted into lambda uni_ZAP XR vector at St. end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression
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/note="Weetor: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Callus was treated with ABA(20um) for lhour. cDNA
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Embrartoidaes; Oryzae, Oryza.

(bases 1 to 9)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTS

Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongGi, Korea
Tel: 82 31 330 6193
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CF325534 9 bp mRNA linear EST 18-AUG-2003 JWT1--03-H24.gl AtJWT-overexpressing transgenic rice lambda phage cDNA library (JWT1) Oryza sativa cDNA clone JWT1--03-H24, mRNA
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XhoI; CDNA was inserted into lambda Uni-ZAP XR vector at
5' end with ECORI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enrhartoidees; Oryzae.

Enrhartoidees; Oryzae.

I (Bases 1 to 9)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.
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1 (bases 1 to 9)

Kim, J.S.; Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                             Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Yeonggi, Korea
Yengin, Xorea
13 33 06193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Yongin, Kyeonggi, Korea
11 31 31 31 6193
Fax: 82 31 321 6355
Email: bhnahm@gdbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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E. L. Bases 1 to 9)

S. Xim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.T., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/clone lib="OsliARC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."
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                                                                                                            Length 9;
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/clone lib="AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1)"
//note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: Xho; FUNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from Arabidopsis Jasmoinate Carboxyl
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1 (Dases 1 to 9)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bloinformatics, MyongJi University
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Ehrhartoideae, Oryzeae, Oryza.
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/dev stage="14 days after germination"
/lab_host="E.coli SOLR"
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Location/Qualifiers
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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phage cDNA library (JMT1)"

/noce="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

Xhof; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site. mRNA was

prepared from Arabidopsis Jasmoinate Carboxyl

methyltransferase overexpression line."
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XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site. mRNA was
prepared from Arabidopsis Jasmoinate Carboxyl
methyltransferase overexpression line."
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Enhratroideae; Oryzeae; Oryza.

Enhratroideae; Oryzeae; Oryza.

Exim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bioinformatics, MyongJi University
YongIn, Kyeonggi, Korea
Tel: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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'organism="Oryza sativa"
'mol_type="mRNA"
'cultivar="Nackdong"
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Best Local Similarity
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Oryza sativa
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Best Local Similarity
Matches 8; Conserv
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CF325534/c DEFINITION

RESULT 78

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ORGANISM

SOURCE

ACCESSION

VERSION KEYWORDS

TITLE JOURNAL COMMENT

REFERENCE AUTHORS ;

Gaps

source

FEATURES

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Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                           CTCGCATCC
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JOURNAL
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                      /dev_srage="14 days after germination"
/lab_host="B.coli SOLR"
/lab_host="B.coli SOLR"
/clone_lib="AtJWI-owrl)
phage CDNA library (JWT1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
Khoi; cDNA was inserted into lamda Uni_ZAP XR vector at 5'
end with EcoRI and 3' end with Xhoi site. mRNA was
prepared from Arabidopsis Jasmoinate Carboxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
711: 610-270-7245
Fax: 610-270-5598
Email: sanjay kumar-1@osk.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
              Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
TyongJn, KyeongJi Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG925375 10 bp mRNA linear EST 06-NOV-20
HNC5-1-A9.R HNC (Human Normal Cartilage) Homo sapiens CDNA, mRNA
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Osteoarthr. Cartil. 9 (7), 641-653 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.3%; Score 7.4; DB 1; Length 9; 88.9%; Pred. No. 1.18+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                              Email: bhnahm@ggbio.com, bhnahm@bio.myongjí.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     methyltransferase overexpression line."
                                                                                                                                                                                                                                                                     /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4530"
/clone="JMT1--03-N02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: sanjay kumar-1@gsk.com
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       'tissue_type="leaf"
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(bases 1 to 9)
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Matches 8; Conserv
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BG925375
                  AUTHORS
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REFERENCE
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Tetrahymena thermophila cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Tetrahymena thermophila"
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/mol type="mRNA"
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/note="Vector: BlueScriptz SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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Turkwaitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
BST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkwaitz AP
Molecular Genetics and Cell Biology
/issue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"
                                                                                                                                                                                                       Gaps
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Tetrahymena thermophila
Tetrahymena thermophila
Bukaryota, Alveolata, Ciliophora, Oligohymenophorea,
Hymenostomatida, Tetrahymenina, Tetrahymena.
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Bukaryota, Alveolata, Ciliophora, Oligohymenophorea,
Hymenostomatida, Tetrahymenina, Tetrahymena.
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88.9%; Pred. No. 22;
tive 0; Mismatches 1; Indels
                                                                                                                                                     Length 10;
                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Chicago
920 E. Sath Street, Chicago, IL 60637, USA
TTEL: 773 702 4374
Fax: 773 702 3172
                                                                                                                                                                                                    1;
                                                                                                                                                     DB 1;
                                                                                                                                                  Score 7.4; DB Pred. No. 22; 0; Mismatches
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Seq primer: T3.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tetrahymena thermophila
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                                                                                                                                                     0.3%;
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Best Local Similarity
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EST 15-AUG-2003
plasmid cDNA
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 10)
1 (bases 1 to 10)
2 (beong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Kim, Y. -K. and Nahm, B. H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                           CF311011
ABF--06-B02.b1 ABF3-overexpressing transgenic rice plasmid cDNA
Library (ABF) Oryza sativa cDNA clone ABF--06-B02, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="14 days after germination"
/lab_host="B.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
                                                                            Gaps
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ABF--06-B02.bl ABF3-overexpressing transgenic rice library (ABF) Oryza sativa cDNA clone ABF--06-B02, CF311011

CF311011.1 GI:33682772
                              Length 10;
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                                DB 1;
                              0.3%; Score 7.4; DB
88.9%; Pred. No. 22;
tive 0; Mismatches
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88.9%; Pred. No. 22;
ative 0; Mismatches
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="ABF--06-B02"
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         8; Conservative
                                                                                                                    1206 CTATCAGGG 1214
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      EST
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                           DEFINITION
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DEFINITION
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                                                                                                                                                                                                                               RESULT 85
CF311011
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                                                                                                                                                                                                                                                                                                                                                   /mol type="mgNA"
/strain="CU428.1"
/db xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pinus sylvestris/Heterobasidion annosum
Pinus sylvestris/Heterobasidion annosum
Eukaryotes, mixed EST libraries.
1 (bases 1 to 10)
Asiegbu,F.O., Nahalkova,J. and Dean,R.A.
Selected Expressed sequence tags of cDNA clones from the
interaction of the root rot fungus (Heterobasidion annosum) with
seedling roots of Scots pine (Pinus sylvestris)
Compublished (2001)
Contact: Fred O. Asiegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel, J. and Klobutcher, L.
Frankel, J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Fax: 773 702 4374
Fax: 773 702 4374
Fax: 773 702 4374
Fax: 773 702 4372
Fax: 773 702 4374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hage005aD02 Heterobasidion annosum - Scots pine infection stage (HAGB) subtraction cDNA library Pinus sylvestris/Heterobasidion annosum cDNA clone hage005aD02, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Pinus sylvestris/Heterobasidion annosum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                  1. .10
/organism="Tetrahymena thermophila"
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88.9%; Pred. No. 22;
tive 0; Mismatches
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Fax: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:169015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: T7 primer.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Best Local Similarity
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SALK 001766 Arabidopsis thaliana TDNA linear GSS 03-OCT-2001 SALK 001766 Arabidopsis thaliana TDNA insertion lines Arabidopsis Ethaliana genomic clone SALK_001766, genomic survey sequence. BH169696
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/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/clone lib="Chilcoat/Turkewitz SK+, Details on library
/note="Vector: BluesCriptz SK+, Details on library
/reparation can be found in Chilcoat and Turkewitz (2001)
/proc. Natl. Acad. Sci USA, 98: 8709-8713."
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Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota: Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.

1 (bases 1 to 11)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
                            |db_xref="taxon:3641"
|/clone="Cac BL 1340"
|/tissuc_type="Mature leef and mature bean"
|/cell_type="maturity"
|/dev_ftage="maturity"
|/lab_host="XL-1 Blue MRF"
|/clone_lib="Cac_BL (Bean and Leaf from Amelonardo type
|Cacao]"
                                                                                                                                                                                                                  'note="Vector: pBK-CMV; Bean and leaf tissue from an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BM395226
50072-2-8-B04.f.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                        Length 10;
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/mol_type="mRNA"
/strain="CU428.1"
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University of Chicago
920 E. 58th Street, Chicago, IL 60637,
Fax: 773 702 3172
                                                                                                                                                                                                                                                                                   11arity 88.9%; Score 7.4; DB Conservative 0; Mismatches
                                                                                                                                                                                                                                          Amelonado type Cacao tree."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: apturkew@midway.uchicago.edu
Seq primer: T3.
           strain="Amelonado type"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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BH169696/C
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Brhatroideae; Oryzeae; Oryza.

1 (Dases 1 to 10)

S Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTS

Unpublished (2003)

Contact Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bioinformatics, MyongJi University
YongJin, KyeongJi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA794390 10 bp mRNA linear EST 05-DEC-2002 Cac_BL_1340 Cac_BL (Bean and Leaf from Amelonardo type Cacao) Theobroma cacao cDNA clone Cac_BL_1340 5', mRNA sequence.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4530"

clone="ABF--06-BD2"

/closue="ABF--06-BD2"

/dev_stage="14 days after germination"

/dev_stage="14 days after germination"

/dev_stage="15.001 bH108"

/clone lib="ABF9-overexpressing transgenic rice plasmid

cDNA library (ABF)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 10)
Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
Retzel, E.R. and Jones, C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                    Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3d Dundee Road, Slough, Berkshire, UK, SL1 4LG Tel: +44 1664 416644
Email: Paul.Jones@eu.effem.com
Seq primer: T3
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/wol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                         organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Planta 216 (2), 255-264 (2002)
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Gaps

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/tissue_type="storage root"
| Lab_host="EMDH10B" |
| Lab_host="EMDH10B" |
| Clone lib="WPL2-ADIS-024-storage root" |
| Intermy from sugar beet, library provided by KWS |
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Makaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Viridiplantae, Streptophyta, Embryophyta, Poaceae, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza, I. (Dasea, I.C.) (Dayza, I.C.) (Man, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTS Unpublished (2003)
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     orientation:
SP6-SalI-CCACGCGCCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Regenerated callus lambda phage cDNA library
                                                                                                                                                                                                                                                     /mol_type="mRNA"
/culTivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prof. Christian Jung; Sequence Survey. RZPD/GABI-Primary database: http://gabi.rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                       Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 12 Std Brror: 0.00
Plate: 17 row: P column: 07
Seg primer: SP6; ÇATACGATTTAGGTGACACTATAG.
                                                                                                                                                                                                                       organism="Beta vulgaris"
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/clone="024-017-P07"
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/clone="RCL1--03-M05"
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/cultivar="Nackdong"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Fax: 00492215062851
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(bases 1 to 12)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Sdarinab,P., Kanternes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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/clone="sALK 001766"
/clone lib="Ārabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
ench of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
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0
                                                                                                                                                                                                                                                                                                                                                Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 658 558 6379
Email: ecker@salk.edu
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
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'mol_type="genomic DNA"
'strain="Columbia 0"
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Large scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Unpublished (2003)
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' and with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"
                                                                                                                                                                                                                                                                                                                                       CF295648 8 bp mRNA linear EST 14-AUG-2003 30DGS--05-K23.gl Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--05-K23, mRNA sequence.
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/dev_stage="30 days after germination"
/lab_host="E.coli DH108"
/clone lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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Location/Qualifiers
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                                                                                                                      0.3%; Score 7; DB 1; Les 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0;
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mol_type="mxNx"
/ullivar="Nackdong"
/db_xref="taxon:4550"
/clone="30DGS--05-K23"
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Glycine.

1 (bases 1 to 8)

Alkharouf,N.W., Khan,R. and Matthews,B.F.

Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
Unpublished (2002)

Contact: Alkharouf, N.W.
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Glycine max (soybean)
Glycine max
Glycine max
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                    1 (bases 1 to 8)
Scheffler, B.E., Huang, S., Liu, X., Nguyen, H., Duke, M. and Stacey, G.
Expressed sequence tags from soybean root hair subtractive cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="root hairs"
/clone_lib="Soybean root hair subtracted cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: root hairs; Vector: pCR2-1 Topo; cDNA ogenerated from soybean root hair tissue treated with Bradyrhizobium japonicum for 3 hours."
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                                                                                                                                                                                                                                                                                                                                                                 Contact: Gary Stacey
University of Missouri
University of Missouri
161 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-4752
Fax: 573-882-0588
Email: staceygemissouri.edu
Single pass sequence
Seq primer: T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
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/organism="Glycine max"
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Fax: 301 504 5728
Email: alkharom@ba.ars.usda.gov.
Location/Qualifiers
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RESULT 95 CF313731/c DEFINITION

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ORGANISM

ACCESSION VERSION KEYWORDS SOURCE TITLE JOURNAL COMMENT

AUTHORS REFERENCE

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1 (bases 1 to 9)
Alkharouf,N.W., Khan,R. and Matthews,B.F.
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
Compublished (2002)
Contact: Alkharouf, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM396043 17-JAN-2002 5009-0-15-H12.t.2 Chilcoat/Turkewitz cDNA (large fraction) Terrahymena thermophila cDNA, mRNA sequence.
                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="Seedlings"
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/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."
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Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
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Hymenostomatida, Tetrahymenina; Tetrahymena.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 B. 58th Street, Chicago, IL 60637,
    CDNA clone D16C10 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Glycine max"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
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/clone="D16C10"
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/cultivar="Peking"
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Tetrahymena thermophila
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                                                CA851674.1 GI:33388467
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Glycine max
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Fax: 773 702 3172
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Cryza sativa
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Cryza sativa
ENKarycota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Enkrartoideae; Oryzae; Diliopsida; Poales; Poaceae;
Enrhartoideae; Oryzae; Dryza.

Schay, S. Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Mahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Upublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 331 6193
Fax: 82 31 331 6193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fissue type="callus"

dev stage="proliferated callus on 2N6 media for 2 weeks"

/lab_nost="E.coll DH10B"

/clone lib="Oscall DH10B"

cDNA lib="Y (HD)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 15-AUG-2003
/db_xref="taxon:3847"
/clone="D12G08"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HD--01-P12.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA clibrary (HD) Oryza sativa cDNA clone HD--01-P12, mRNA sequence. CF313731 GI:33685492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Wectór: pCR4-TOPO; Site 1: ECORI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR: mRNA was derived from rice Histone Deacetylase overexpression line."
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    Location/Qualifiers
                                                                                                                                                                                                                                1; Indels
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                                                                                                                                                                                       Length 8;
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Pred. No. 1.3e+02;
0; Mismatches 1;
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/mol_type="mRNA"
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clone="HD--01-P12"
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Best Local Similarity 87.5.
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Source

FEATURES

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RESULT 96 CA851674/c

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/mol_type="mRNA"
/cultivar="Nackdong"
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Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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1. (bases 1 to 10)

Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel,J. and Klobutcher,L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells Unpublished (2002)
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/organism="Tetrahymena thermophila"
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/strain="CU428.1"
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Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637,
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.3%; Score 7; DB 1; Best Local Similarity 100.0%; Pred. No. 37; Matches 7; Conservative 0; Mismatches
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7; Conservative
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta; Liliopsida, Poales, Poaceae; Enrhartoideae, Oryza.

El (Dases I to 10)

S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel. 82 31 320 6193
Fax: 82 31 320 6193
Fax: 82 31 320 6193
Fax: Bemail: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Oryza sativa"
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Xhol; cDNA was inserted into lambda Uni-ZAP XR vector at Sf. end with EcoRI and 3' end with Xhol site. mRNA was derived from rice Histone Deacetylase overexpression
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10 bp mRNA linear EST 18-AUG-2002

HDN--05-A22.g1 OsHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--05-A22, mRNA
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzaee, Dryza.

1 (bases 1 to 10)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Fax: 82 31 321 6355
Bmail: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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100.0%; Pred. No. 37;
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Best Local Similarity 100.0%; Pred. No. 37;
Connectvative 0; Mismatches
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EST 17-JAN-2002
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HNC1-1-G11.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:5911"
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/clone lib="Chilcoat/Turkewitz SK+, Details on library
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Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
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709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                    Tetrahymena thermophila
Tetrahymena thermophila
Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.

1. (bases 1 to 11)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
Frankel, J. and Kiboutcher, L.
Errankel, J. and Kiboutcher, L.
Errankel, Compublished (2002)
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                    BM395228
50072-2-8-B05.r.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .11
/organism="Tetrahymena thermophila"
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/strain="CU428.1"
                                                                                                                                                                                                                                                                                                                                                                              Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
                                                                                                                        BM395228.1 GI:18195281
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COMMENT
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Ehrhartoldeae; Oryzae; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzae; Liliopsida; Poales; Poaceae;
Enthartoldeae; Oryzae; Liliopsida; Poales; Poaceae;
Enthartoldeae; Oryzae; Liliopsida; Lee,T.H., Shin,Y.C.,
Song, S.I., Kim,J.K., Cheong, T., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song, S.I., Kim,J.K., Kim,Y.-K. and Nahm, B.H.
Gong, S.I., Kim,J.K., Kim,Y.-K. and Nahm, B.H.
Gontact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Biosecience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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10 bp mRNA linear BST 18-AUG-2003
JMT--07-C04.gl AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--07-C04, mRNA sequence.
               /tissue_type="callus"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone lib="OSHDAC1-overexpressing transgenic rice lambda
plage cDNA library II (HDN)"
/note="Voctor: pBluescript SK(+); Site 1: BcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
S. end with BcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."
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Location/Qualifiers
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100.0%; Pred. No. 37;
tive 0; Mismatches 0; Indels
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CF336905.1 GI:33822181
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CF336905
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Fax: 610-270-5598

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CF282215.1 GI:33659602
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Matches 7; Conservative
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HNC45-1-D11.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Detheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 11)

Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlaxoSmithKline
Yos Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7345
Fax: 610-270-5598
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                                                           /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxnon:9606"
/lisume type="cartilage"
/lab_host="E.coli DH10 B"
/clone lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT I; Site_1: Sall; Site_2: NotI;
                                                                                                                                                                                                                                                      Gaps
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/clome lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT I; Site_1: Sal1; Site_2: Not1;
Directional"
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5. 62;
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100.0%; Pred. No. 62;
iive 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches
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/db_xref="taxon:9606"
/tissue_type="cartilage"
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Email: sanjay kumar-1@gsk.com
Seq primer: T7.
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Seq primer: T7.
          Seq primer: T7.
Location/Qualifiers
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BG927896.1 GI:14322419
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Best Local Similarity 100.
Matches 7; Conservative
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RESULT 105

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Dryzaa.

El (baees 1 to 11)

S Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.T., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggblo.com, bhnahm@blo.myongji.ac.kr.
CF323154

11 bp mRNA linear EST 18-AUG-2003

HDN--03-B04.gl OSHDACl-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--03-B04, mRNA
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab host="E.coli SOLR"
/clone_lib="OBHDACI-Overexpressing transgenic rice lambda
phage CDNA lib="OBHDACI-Overexpressing transgenic rice lambda
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 12)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.L., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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100.0%; Pred. No. 62;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/cultivar="Nackdong"
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schultz451-1.rst

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Circa Saciary Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bhrhartoideae; Oryzeae; Oryza.

El (Dases I to 10)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 bp mRNA linear EST 18-AUG-2003 JMT--07-C04.gl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--07-C04, mRNA sequence.
                                                                                                                                                                              CF333615

10 bp mRNA linear EST 18-AUG-2003

JMT--02-J09.gl AtJMT-overexpressing transgenic rice plasmid cDNA

Library (JMT) Oryza sativa cDNA clone JMT--02-J09, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCR4-TOPO, Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Shrhartoidee, Oryzeae, Oryza.

1 (Dases 1 to 10)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K. and Nahm,B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | db xref="taxon:4550"
| clone="JMT--02-J09"
| fissue type="leaf"
| dev stge="14 days after germination"
| lab_host="E.coli DH10B"
| clone lib="AtJMT-overexpressing transgenic rice plasmid
| clone lib="AtJMT-overexpressing transgenic rice plasmid
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80.0%; Pred. No. 46;
7ative 0; Mismatches 2; Indels
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/mol type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                    CF333615.1 GI:33815525
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                               77 AGGAGGGAG 86
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Best Local Similarity
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SOURCE
ORGANISM
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CF336905/c
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ORGANISM
                                                                                                                                                            CF333615/c
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                                                                                                                                     RESULT 108
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JOURNAL
COMMENT
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KEYWORDS
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Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonuclectides and Then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG925375 10 bp mRNA linear EST 06-NOV-20
HNC5-1-A9.R HNC (Human Normal Cartilage) Homo sapiens CDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries 05teoarthr. Cartil. 9 (7), 641-653 (2001)
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                                                                                                                                                                                                                                                                                                        /clone lib="Rice etiolated leaf plasmid cDNA library (14ETL)^{-1}"
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/lab host="E.coli DH10 B"
/lobe="ware" (Human Normal Cartilage)"
/hote="Wector: pSPORT 1; Site_1: Sal1; Site_2: Not1;
/birectional"
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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. 78;
                                                                                                                                                                                                                                                                  germination"
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                                                                                                                                                                                         /db_xref="teaxon:4530"
/clone="14ETL--09-K01"
/tissue_type="leaf"
/dev_stage="14 days after ge
/lab_host="E.coli DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                                     0.3%; Score 7; DB 1
100.0%; Pred. No. 78;
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                 organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay kumar-l@gsk.com
Seq primer: T7.
                                                                                                                                                   /mol_type="mRNA"
/cultivar="Nackdong"
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BG925375.1 GI:14319898
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UW2109
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Similarity 80.0%;
8; Conservative
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Best Local Similarity 100.0
17, Conservative
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Best Local Similarity
Matches 8; Conserv
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KEYWORDS
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MEDLINE
PUBMED
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/clone lib="MPIZ_ADIS-024-storage root" / clone lib="MPIZ_ADIS-024-storage root" / force="Vector: pCMVSPORT6; Site 1: Sal1; Site 2: Not1; CDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
                                                                                                                                                                                                                                   orientation:
Sep6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Notl-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local P1: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 18-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HDN--01-M19.91 OsHDAC1-overexpressing transgenic rice lambda phage CDNA library II (HDN) Oryza sativa CDNA clone HDN--01-M19, mRNA
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="OsHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN)" | //note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim, N.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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0.3%; Score 6.8; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 72;
Matches 8; Conservative 0; Mismatches 2; Indels
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Pred. No. 72;
0; Mismatches
                                                                   'tissue_type="storage_root"
'lab_host="EMDH10B"
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/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="callus"
                                              clone="024-018-024"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CF322692.1 GI:33793616
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
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E012597-024-018-024-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
CDNA clone 024-018-024 5-PRIME, mRNA sequence.
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(aryophyllales; Amaranthaceae; Beta.

(bases 1 to 11)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
                    Unpublished (2003)
Contact: Nahm B.H.
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="leaf"
/dev stage="14 days after germination"
/lab_host="E.coll DH10B"
/clone lib="AtJWT-overexpressing transgenic rice plasmid
cDNA library (JWT)"
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
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                                                                                                                                                                                               Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
Location/Qualifiers
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ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
     Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 11 Std Error: 0.00
Plate: 18 row: 0 column: 24
Seq primer: SP6; CATACGATTTAGGTGACATATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 6.8; DB
Pred. No. 46;
0; Mismatches
                                                                                                                                                                                                                                                                          /organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db zref="taxon:4130"
/clone="JMT--07-C04"
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Beta vulgaris
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schultz451-1.rst

GSS 03-0CT-2001

LOCUS RESULT 112

AQ050979

qq à

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE

REFERENCE

JOURNAL

COMMENT

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/mol type="ganomic DNA"
/strain="Columbia 0"
/db xref="texton:3702"
/clone="SALK_001378"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Theobroma cacao cDNA clone Cac_BL_611 5', mRNA sequence.
                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids; Li Brassicales; Brassicales; Brabidopsis.
                                                                        вн1/0808 13 bp DNA linear GSS 03-ОСТ-200
SALK 003378 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK 003378, genomic survey sequence.
BH170808
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A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome Unpublished (2001)
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Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
Retzel, E.R. and Jones, C.A.
Gene discoverty and microarray analysis of cacao (Theobroma cacao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is single pass sequence recovered from the left border of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Joseph R. Bcker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
TH: 858 453 4100 x1752
Fax: 858 6379
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    13
/organism="Arabidopsis thaliana"

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Arabidopsis thaliana (thale cress)
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/db_xxef="taxon:3994"
/db_xxef="taxon:3994"
/clone="nbx0004H22"
/fissue type="Leaf"
/lab_host="e.coli DH10B"
/clone=lb="CudI Rice BAC Library"
/clone=lb="CudI Rice BAC Library"
/clone=lb="CudI Rice BAC Library"
/note="Wector: pBeloBAC11; Site 1: HindIII; Site 2:
HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbotydrate. Monocctyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
                                                                                                                                                                                             AQU50979 linear GSS 24-WAR-1999
nbxb0004dDllr CUGI Rice BAC Library Oryza sativa (japonica
cultivar-group) genomic clone nbxb0004H22r, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
Gases I to 12)
Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1198)
On Mar 23, 1999 this sequence version replaced gi:3325284.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemson University Genomics Institute Clemson University Genomics 29634, USA 100 Jordan Hall, Clemson, SC 29634, USA 161: 864 656 7288
Fax: 864 656 4293
Small: rwing@clemson.edu
Seq primer: GGaAACAGCTATGACCATG
Class: BAC ends
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Pred. No. 82;
0; Mismatches
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/strain="Japonica"
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1494 GCGCGAGGCC 1503
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                                                   1 GCACGAGGC 10
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Best Local Similarity
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EST 15-AUG-2003
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Brhatroideae; Oryzaae; Oryza.

1 (bases 1 to 8)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice BSTs
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Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
      /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: Xho1; Leaf was dried for 2hrs. cDNB was inserted into—lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNB was prepared from ABA-responsive element binding transcription factor 3 overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="ABF9-overexpressing transgenic rice lambda phage cDNA library (ABF1)"
| Inote="Vector: pBluescript SK(+); Site 1: EcoR1; Site 2: Xho1; Leaf was dried for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoR1 and 3' end with Xho1 site. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                    ABF1--06-009.gl ABF3-overexpressing transgenic rice lambda phage cDNA library (ABF1) Oryza sativa cDNA clone ABF1--06-009, mRNA
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                                                                                                                                              Length 8;
                                                                                                                                            Score 6.4; DB 1; Length 8;
Pred. No. 1.3e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                   linear
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/mol_type="mRNA"
culfivar="Nackdong"
/db xref="taxon:4530"
/clone="ABF1--06-009"
/tissue_type="leaf"
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/lab_host="E.coli SOLR"
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Pred. No. 1.3e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                   mRNA
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CF305141.1 GI:33676902
                                                                                                                                          0.3%;
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Best Local Similarity 87.5%;
Matchès 7; Conservative
                                                                                                                       Query Match
Best Local Similarity 87.5.
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                                                                                                       line."
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1 (bases 1 to 8)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABF1--06-009.gl ABF3-overexpressing transgenic rice lambda phage cDNA library (ABF1) Oryza sativa cDNA clone ABF1--06-009, mRNA
                                                                                                                                                                                                                                                                                                                                    /tissue_type="Mature leaf and mature bean"
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/dev_stage="maturity"
/lab_host="XL-1 Blue MRF'"
/clab_host="XL-1 Blue MBF'"
/clab_host="XL-1 Blue MBF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar=Nackdong"
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/lab_host="E.coli SOLR"
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phage CDNA library (ABF1)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 14;
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                                                                                             Masterfoods
3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
Email: Paul.Jones@eu.effem.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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                                                                                                                                                                                                                                       organism="Theobroma cacao"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amelonado type Cacao tree.
                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="Amelonado type"
/db_xref="taxon:3641"
/clone="Cac_BL_611"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 6.8;
Pred. No. 73
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L.) varieties
Planta 216 (2), 255-264 (2002)
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CF305141.1 GI:33676902
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Contact: Jones, Paul
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Best Local Similarity 80.0
Matches 8; Conservative
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CF306762 8 bp mRNA linear EST 15-AUG-2003 HDA1--04-M13.gl OsHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDA1) Oryza sativa cDNA clone HDA1--04-M13, mRNA
                                                                                                                                                                                                                                               /tissue type="rollus"
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/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Callus was treated with ABA(20um) for lhour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
ECORI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaee; Oryza
I (bases 1 to 8)
Kim,J.S., Jun, K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2001)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bloinformatics, MyongJi University
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0
  Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.3%; Score 6.4; DB 1; Length 8; 87.5%; Pred. No. 1.3e+02; rative 0; Mismatches 1; Indels
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                                                                                                                            /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Oryza sativa"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Best Local Similarity 87.5
Matches 7; Conservative
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phage cDNA library I (HDA1)"
//done library I (HDA1)"
/done: "Bluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Callus was treated with ABA(20um) for lhour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."
                                                                                                                                                              SM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enthattoldeae; Oryzae; Circonae; Liliopsida; Liliopsidae; Liliopsidae; Liliopsidae; Circonae; Man, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Lonpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Rioscience and Bioinformatics, Myongdi University
Yongin, Kyenonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
HDA1--02-L22.gl OsHDACl-overexpressing transgenic rice lambda phage cDNA library I (HDA1) Oryza sativa cDNA clone HDA1--02-L22, mRNA
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1 (Bases 1 to 8)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Darge-scale Sequencing Analysis of Rice BSTs

Contact: Nahm B.H.
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Location/Qualifiers
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/organism="Oryza sativa"
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/db_xref="taxon:4530"
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CF306116/c
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FEATURES

REFERENCE AUTHORS

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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bhrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 8)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="callus"
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/lab_nost="E.coll SOLR"
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phage cDNA library II (HDN)" (+); Site 1: ECORI; Site 2:
/note="Vector: pBluescript SK(+); Site 1: ECORI; Site 2:
Xho1; CDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with Xho1 site. mRNA was
derived from rice Histone Deacetylase overexpression
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HDN--01-E13.gl OsHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--01-E13, mRNA
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1. (bases 1 to 8)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.
                                                                                                                                                                                                                                         Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Oryza sativa"
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Location/Qualifiers
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Dryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Epkaryota; Viridiplantae; Streptophyta; Enkaryota; Poaceae; Enkartoideae; Oryzae; Oryzae; CE

I (bases 1 to 8)

RS Xim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTS

Ontact: Nahm B.H.

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YongIn, Kyeonggi, Korea

Tel: 82 31 321 6555

Email: bhnahm@ggbbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                        CF306762 B bp mRNA linear EST 15-AUG-2003
HDA1--04-M13.gl OsHDACl-overexpressing transgenic rice lambda phage
CBNA library I (HDA1) Oryza sativa cDNA clone HDA1--04-M13, mRNA
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B bp mRNA linear EST 18-AUG-2003
HDN--01-E13.91 OSHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--01-E13, mRNA
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                           0.3%; Score 6.4; DB 1; Length 8; 87.5%; Pred. No. 1.3e+02; ive 0; Mismatches 1; Indels
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CF306762.1 GI:33678523
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CF322514.1 GI:33793267
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Best Local Similarity 87.5-
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DEFINITION

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RESULT 121

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EST 18-AUG-2003
                                                                                                                                                                           HDN--01-K24.g1 OsHDAC1-overexpressing transgenic rice lambda phage CDNA library II (HDN) Oryza sativa CDNA clone HDN--01-K24, mRNA
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Burhartoideae; Oryzae; Oryza.

I (bases 1 to 8)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Xim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site 1: EcoR1; Site 2:
Xho1; cDNA was inserted into lambda Uni-ZAP XR vector at
derived from rice Histone Deacetylase overexpression
line."
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8 bp mRNA linear EST 18-AUG-2003
HDN--05-A16.gl OsHDAC1-overexpressing transgenic rice lambda phage
CDNA library II (HDN) Oryza sativa cDNA clone HDN--05-A16, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Bioinformatics, MyongJi University
Yorgin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Bmail: bhnahm@ggblo.com, bhnahm@blo.myongji.ac.kr.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermacophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 8)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K. Kim,Y.-K. and Nahm,B.H.
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                                                                                                                                                        mRNA
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/db xref="taxon:4530"
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CF322653.1 GI:33793540
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8 bp mRNA linear EST 18-AUG-2003
HDN--01-K24.gl OSHDACl-overexpressing transgenic rice lambda phage
CDNA library II (HDN) Oryza sativa CDNA clone HDN--01-K24, mRNA
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1. (bases 1 to 8)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song, S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTS

Contact: Nahm B.H.
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/lab_host="B.coll SOLR"
/clone_lib="0.9HDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
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Yorgin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6555
Email: bhnahm@gdpio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
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clone="HDN--01-K24"
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EST

KEYWORDS SOURCE

ACCESSION VERSION

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

DEFINITION

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FEATURES

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Query Match

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1 (Dases 1 to 8)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
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XhoI; CDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
          phage cDNA library II (HDN)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."
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Tel: 82 31 330 6133
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com_bhnahm@bio.myongji.ac.kr.
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0; Mismatches 1;
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Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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8 bp mRNA linear EST 18-AUG-2003 HDN--05-Al6.gl OSHDACl-overexpressing transgenic rice lambda phage CDNA library II (HDN) Oryza sativa cDNA clone HDN--05-Al6, mRNA
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fnote="Woctor: pBluescript SK(+); Site_1: EcoRI; Site_2: Ahol: cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with Xhol site. mRNA was derived from rice Histone Deacetylase overexpression
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                                                                        GreenGene Biotech Inc.; Division MyongJi University
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                 Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech
Genomics and Genetics Institute, GreenGene Biotech
Genomics and Bioinformatics, MyongJi Universit
Yongin, Kyeonggi, Korea
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Fax: 82 31 321 6355
Email: bhnahm@ggblo.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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     Large-scale Sequencing Analysis of Rice ESTs
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87.5%; Pred. No. 1.3e+02;
Live 0; Mismatches 1
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Matches 7; Conservative
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/dev stage="14 days after germination"
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phage cDNA library (JMT1)"
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phage cDNA library (JMT1)"
/clone lib="AtuMT-verexpressing transgenic rice lambda
phage cDNA library (JMT1)"
/clone lib="AtuMT-verexpression line."
xhol; cDNA was inserted into lamda Uni=ZAP xR vector at 5'
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prepared from Arabidopsis Jasmoinate Carboxyl
methyltransferase overexpression line."
                                                                                                                                                                                                                                                        /tissue type="14" days after germination"

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phage cDNA lib=ary (JMT1)"

/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:

Xhol; cDNA was inserted into landa Uni-ZAP XR vector at 5'

end with EcoRI and 3' end with Xhol site. mRNA was

prepared from Arabidopsis Jasmoinate Carboxyl

methyltransferase overexpression line."
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8 bp mRNA linear EST 18-AUG-2003 JMT1--03-B08.gl AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-B08, mRNA
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1 (bases 1 to 8)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
                      Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
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                                                                                                                                organism="Oryza sativa"
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/clone="JMT1--03-B08"
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/db_xref="taxon:4530"
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Location/Qualifiers
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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1. (bases 1 to 8)

2. Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

1. Large-scale Sequencing Analysis of Rice ESTs

Contact: Nahm B.H.

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Large-scale Sequencing Analysis of Rice ESTs
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Ensocience and Bioinformatics, MyongJi University
YongJin, Kyeonggi, Korea
Tel: 82 31 330 6193
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B bp mRNA linear EST 18-AUG-200
JMT1--03-B08.gl AtJMT-overexpressing transgenic rice lambda phage
cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-B08, mRNA
cDNA library II (HDN) Oryza sativa cDNA clone HDN--06-H05, mRNA
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                                                                             CF324406.1 GI:33797080
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/mol_type="mRNA"
/cultivar="Nackdong"
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phage cDNA library (JMT1)" (Stell: EcoRI; Site 2:
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; CDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site. mRNA was
prepared from Arabidopsis Jasmoinate Carboxyl
methyltransferase overexpression line."
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1 (Dases 1 to 8)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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B bp mRNA linear EST 18-AUG-2003 JMT1--03-F06.gl AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-F06, mRNA
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WT1--03-F06.gl AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-F06, mRNA
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                     Score 6.4; DB 1; Length 8; Pred. No. 1.38+02; 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Best Local Similarity 87.5%; Pred. No. 2.2.2
Matches 7; Conservative 0; Mismatches
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/mol_type="mRNA"
/cultivar="Nackdong"
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CF325469.1 GI:33799223
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Query Match
Best Local Similarity 87.5
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CF325469/c
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AUTHORS
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JOURNAL
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Orygas sativas
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Enkartoidea; Orygae; Orgae; Orygae; Orgae; Or
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Bukaryota, Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Buthartoideae; Oryzeae; Oryza.
1 (bases 1 to 8)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Nahm B.H. GreenGene Biotech Inc., Division of Bloscience and Bioinformatics, MyongJi University
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Whith--03-F22.gl AtUMT-overexpressing transgenic rice lambda phage cDNA library (JMI1) Oryza sativa cDNA clone JMI1--03-F22, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
    Location/Qualifiers
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0.3%; Score 6.4; DB 1;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1;
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT1--03-F06"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Exaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhattoideae; Oryzeae; Oryza.

1 (bases 1 to 8)

2 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTS
Uppublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongdi University
Yongin, Kyeongqi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBluescript SK(+); Site_1: SstI; Site_2: Khol; cDNA was inserted into landa Uni-ZAP XR vector at 5' end with SstI and 3' end with Xhol site. Callus was induced on 2Ne media for 30 days and cultured for 36hrs on
                                                                                                                        CF338362 8 bp mRNA linear EST 18-AUG-2003
RCL1--01-H06.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa cDNA clone RCL1--01-H06, mRNA sequence.
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Ehrhartoidaes; Oryzae; Oryzae.

(Dases 1 to 8)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.
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/cultivar="Nackdong"
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Location/Qualifiers
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                                                                RESULT 135
CF338362/c
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AUTHORS
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JOURNAL
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/db_xref="taxon:4530"
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/tissue_type="leaf"
/dev stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="ALUMT-overexpressing transgenic rice lambda phage cDNA library (JMT1)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: Xhol; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with Xhol site. mRNA was prepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
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8 bp mRNA linear EST 18-AUG-2003
JMT1--03-F22.gl AtJMT-overexpressing transgenic rice lambda phage
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1 (bases 1 to 8)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yorgin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongJi.ac.kr.
Location/Qualifiers
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/lab_host="E.coli_SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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CF325485.1 GI:33799255
                                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
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Oryza sativa
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Best Local Similarity
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RESULT 134 CF325485/c LOCUS DEFINITION

Matches

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SOURCE ORGANISM

ACCESSION VERSION KEYWORDS REFERENCE AUTHORS

TITLE JOURNAL

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induced on 2N6 media for 30 days and cultured for 36hrs on
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gmrhRww3-10_B07_1_061 Soybean root hair subtracted cDNA library
GTP21494
CF921494.1 GI:38192288
EST.
                                                                                                                                                                                                                                                                                                                            CF340204 BD mRNA linear EST 18-AUG-2003 RCL1--07-E15.gl Regenerated callus lambda phage cDNA library (RCL1) Oryza sativa cDNA clone RCL1--07-E15, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales; Poaceae, Enrhartoideae; Oryzeae; Oryza.

1. (baess 1 to 8)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.T., Kim,J.K., Xim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/down=lib="Regenerated callus lambda phage cDNA library
(RCL1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University YongJu, KyeongJi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnalm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                        Gaps
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                                                                                                                                     0;
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                                                                                            Length 8;
                                                                                   Score 6.4; DB 1; Length 8;
Pred. No. 1.3e+02;
0; Mismatches 1; Indels
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7; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4530"
/clone="RCL1--07-E15"
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/cultivar="Nackdong"
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                                              regenerated media"
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                                                                                     0.3%;
                                                                                                                               7; Conservative
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CF921494/c
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RCL1--05-K22.gl Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa cDNA clone RCL1--05-K22, mRNA sequence,
                                                                                                                                                                                                                                                                                                                dev_stage="proliferated callus on 2N6 media for 30 days" lab_host="E.coli SOLR"
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University vorgin, Kyeongqi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enrhartoideae; Oryzaa.

1 (Dases 1 to 8)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Nahm B.H.

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

YongJi, KyeongJi, Korea

Tel: 82 31 330 6193

Fax: 82 31 31 221 6355

Email: bhnahm@ptio.com, bhnahm@btio.myongji.ac.kr.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        clone lib="Regenerated callus lambda phage cDNA library
อกาก"
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Pred. No. 1.3e+02;
0; Mismatches 1; Indels
                                                                                                                                                                          /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                             db_xref="taxon:4530"
clone="RCL1--03-111"
                                                                                                                                                                                                                                                                                            tissue_type="callus"
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/clone="RCL1--05-K22"
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Best Local
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CA794554

8 bp mRNA linear EST 05-DEC-2002
Cac_BL_1496 Cac_BL (Bean and Leaf from Amelonardo type Cacao)
Theobroma cacao cDNA clone Cac_BL_1496 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Theobroma cacao
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 8)
Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
Retzel, E.R. and Jones, C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao
                                /clone="Cac_BL_1496"
/tissuc_type="Mature leaf and mature bean"
/call type="Whole organ"
/dev_stage="maturity"
/lab_host="Xi-1 Blue MRP""
/clone lib="Cac_BL (Bean and Leaf from Amelonardo type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="Amelonado type"
/strain="Amelonado type"
/db xref="taxon:3641"
/clone="Cac_BL1496"
/clone="Rac_BL="Mature leaf and mature bean"
/cell_type="Maturity"
/dev_stage="maturity"
/lab_host="XL-1 Blue MRF'"
/clone="Laboration of the cap of the cac Blue MRF'"
/clone="XL-1 Blue MRF'"
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                                                                                                                                                                             /note="Vector: pBK-CMV; Bean and leaf tissue from Amelonado type Cacao tree."
                                                                                                                                                                                                                                        Query Match
0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
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/organism="Theobroma cacao"
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Email: Paul.Jones@eu.effem.com
Seg primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Planta 216 (2), 255-264 (2002) 22337596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA794554.1 GI:26051630
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ORGANISM
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COMMENT
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KEYWORDS
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               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                               Glycine.

(Lobase 1 to 8)
Scheffler, B.E., Huang, S., Liu, X., Nguyen, H., Duke, M. and Stacey, G. Expressed sequence tags from soybean root hair subtractive cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene discovery and microarray analysis of cacao (Theobroma cacao
                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
cultivar="Williams 82"
/db xref="taxon:3847"
/tissue_type="root hairs"
/clone_lib="Soybean root hair subtracted cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: root hairs; Vector: pCR2-1 Topo; cDNA ogenerated from soybean root hair tissue treated with Bradyrhizobium japonicum for 3 hours."
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Cac_BL_1496 Cac_BL (Bean and Leaf from Amelonardo type Cacao)
Theobroma cacao cDNA clone Cac_BL_1496 5', mRNA sequence.
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3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
                                                                                                                                                                                                     Contact: Gary Stacey
University of Missouri
University of Missouri
Tel: 573-884-4752
Fax: 573-882-0588
Email: staceyg@missouri.edu
Single pass sequence
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/organism="Theobroma cacao"
/mol_type="mRNA"
/strain="Amelonado type"
                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Glycine max"
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Email: Paul.Jones@eu.effem.com
Seq primer: T3.
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Planta 216 (2), 255-264 (2002)
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                                                                                                                                                                  library
Unpublished (2003)
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Best Local Similarity 87.5
Matches 7; Conservative
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CA794225

Cac_BL_1208 Cac_BL (Bean and Leaf from Amelonardo type Cacao)
Theorem cacao cDNA clone Cac_BL_1208 5', mRNA sequence.
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/dev stage="proliferated callus on 2N6 media for 2 weeks"

/dev stage="proliferated callus on 2N6 media for 2 weeks"

/dev stage="proliferated callus on 2N6 media for 2 weeks"

/dev stage="proliferated callus"

/dev stage="proliferated callus"

/der stage="proliferated callus"

/doc="weeks"

/der stage="proliferated callus"

/der stage="proliferated callu
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
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1 (basés 1 to 9)
Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
Retzel, E.R. and Jones, C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="Whole organ"
/dev_stage="maturity"
/lab_host="XL-1 Blue MRF""
/clone lib="Cac_BL (Bean and Leaf from Amelonardo type
cacao)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 6.4; DB 1; Length 9; Pred. No. 1.1e+02; 0; Mismatches 1; Indels
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3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
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                                                                                                                          /organism="Oryza sativa"
/mol type="mRNA"
/cullivar="NacKdong"
/db xref="taxon:4530"
/clone="HDN--03-P21"
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/strain="Amelonado type"
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Seg primer: T3.
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Planta 216 (2), 255-264 (2002)
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Best Local Similarity 87.5%;
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CA794225/c
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D06G10_G10_14.abl cDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone D06G10 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 9)
Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean Unpublished (2002)
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9 bp mRNA linear EST 18-AUG-2003 HDN--03-P21.gl OsHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--03-P21, mRNA
                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Alkharouf, N.W.
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnolicophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.

(bases 1 to 9)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Man,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Joseience and Bioinformatics, MyongJi University
YongJi, Kyeonggi, Korea
Tel: 82 31 330 6193
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Pred. No. 1.18+02;
0; Mismatches 1; Indels
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Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
Location/Qualifiers
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clone="D06G10"
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/cultivar="Peking"
                                                                                                                                                         CA850813.1 GI:33387606
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CF323490.1 GI:33795236
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Glycine max
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Best Local Similarity
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Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode Uppublished (2002)
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9 bp mRNA linear EST 15-AUG-2003 HDAL--05-H11.gl OsHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDAl) Oryza sativa cDNA clone HDA1--05-H11, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   o;
                                                                                                          Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="Roots"
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extracted from Peking roots 2 and 4 days past invasion."
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1 (bases 1 to 9)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Contact: Nahm B.H.
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/dev stage="proliferated callus on 2N6 media for 2 weeks"
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/clone lib="05HDAC1-overexpressing transgenic rice lambda
phage cDNA library I (HDA1)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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0.3%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                  Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
Location/Qualifiers
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CF307008.1 GI:33678769
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D07H02_014_15.abl cDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone D07H02_5', mRNA sequence.
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Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean unfected by the soybean cyst nematode
Unpublished (2002)
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D07H02 014_15.abl cDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone D07H02 5', mRNA sequence.
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Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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mol type="mRNA"
cultiva=="peking"
db zref="taxe="peking"
clone="D07H02"
/fissue type="Roots"
/dev stage="seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
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  1larity 0.3%; Score 6.4; DB 1; Length 9; Conservative 0; Mismatches 1; Indels
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0.3%; Score 6.4; DB 1;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1;
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Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
Location/Qualifiers
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RESULT 148 CF307008/c LOCUS DEFINITION

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SOURCE ORGANISM

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TITLE JOURNAL COMMENT

REFERENCE AUTHORS

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ABF--03-C20.bl ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--03-C20, mRNA sequence. CF309109.1 GI:33680870
                                                                                             Oryza sativa
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Brhartoideae; Oryzae; Oryza.
1 (bases 1 to 9)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.L., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Cloue_libe_compart_(RDA1) "

// Note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:

// Note="Vector: created with ABA/Sloum) for Ihour. cDNA

was inserted into lambda Uni-ZAP XR vector at 5' end with

EcoRI and 3' end with XhoI site. mRNA was derived from

rice Histone Deacetylase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev stage="proliferated callus on 2N6 media for 2 weeks"
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/clone_lib="OsHDAC1-overexpressing transgenic rice lambda
                                                                                                                                                                                                                                                                                                      Contact: Nahm B.H.

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bhnahm@pio.myongji.ac.kr.

Location/Qualifiers
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryzae.

(bases 1 to 9)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
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Fax: 82 31 321 6355
Email: bhuahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Best Local Similarity 87.5%;
Matches 7; Conservative
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phage cDNA library I (HDA1)"

/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:

XhoI; Callus was treated with ABA(20um) for lhour. cDNA

was inserted into lambda Uni-ZAP XR vector at 5' end with

EcoRI and 3' end with XhoI site. mRNA was derived from
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9 bp mRNA linear EST 15-AUG-2003
HDAl--05-H11.gl OsHDACl-overexpressing transgenic rice lambda phage
cDNA library I (HDAl) Oryza sativa cDNA clone HDAl--05-H11, mRNA
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HDA1--05-L14.gl OSHDACl-overexpressing transgenic rice lambda phage
CDNA library I (HDA1) Oryza sativa CDNA clone HDA1--05-L14, mRNA
was treated with ABA(20um) for lhour, cDNA into lambda Uni-ZAP XR vector at 5' end with end with XhoI site. mRNA was derived from
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                                                                                                                                                                  Gaps
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                                                                       Deacetylase overexpression line."
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                                                                                                             Score 6.4; DB 1; Length 9;
Pred. No. 1.1e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.3%; Score 6.4; DB 1; Length 9; 87.5%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF307008
CF307008.1 GI:33678769
                       was inserted
EcoRI and 3'
  xhol; Callus
                                                                  rice Histone
                                                                                                             0.3%;
                                                                                                         Query Match 0.3
Best Local Similarity 87.5
Matches 7; Conservative
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source

FEATURES

RESULT 149 CF307092/c LOCUS

Matches

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Gaps

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source

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CF323636

9 bp mRNA linear EST 18-AUG-2003 HDN--04-F24.gl OSHDACl-overexpressing transgenic rice lambda phage CDNA library II (HDN) Oryza sativa CDNA clone HDN--04-F24, mRNA
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JMT1--03-L16.gl AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-L16, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue type="cailus"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/deb_host="R.coli SOLR"
/clone lib="OshDaci-overexpressing transgenic rice lambda
phage cDNA library II (HDN)" (%); Site 1: ECORI; Site 2:
/hote="Voctor: pBluescript SK(+); Site 1: ECORI; Site 2:
XhoI; CDNA was inserted into lambda Uni-zAP XR vector at
5' end with ECORI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza.
I (bases 1 to 9)
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Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="HDN--04-F24"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                     CF323636.1 GI:33795531
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Matches 7; Conserv
             442 CACAAAGG
                                                           2 CACAAGGG
                                                                                                                                                                                                                                                                          sequence.
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ORGANISM
                                                                                                                                      RESULT 152
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JOURNAL
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KEYWORDS
SOURCE
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1 (Dases 1 to 9)

S Kim, J.S., Jun.K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 21 321 6355
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9 bp mRNA linear EST 18-AUG-2003
HDN--04-F24.91 OSHDAC1-overexpressing transgenic rice lambda phage CDNA library II (HDN) Oryza sativa CDNA clone HDN--04-F24, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="osHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) " phage cDNA library II (HDN) " forte="vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."
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dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli_SOLR"
                                                                                                                                                                                                                                                    /note="Vector: pCR4-TOPO; Site_1: BcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression
                                                                                              /clone="ABF--03-C20"
/tissue type="laaf"
/tissue type="laaf"
/dev_stage="14 days after germination"
/lab_host="8.coli DH108"
/clone lib="ABF'-overexpressing transgenic rice plasmid cDNA library (ABF)"
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87.5%; Pred. No. 1.1e+02;
Mismatches 1; Indels
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0.3%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
'organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN--04-F24"
                        /mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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CF323636.1 GI:33795531
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Best Local Similarity 87.5-
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LOCUS RESULT 151

CF323636

ð g ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

TITLE JOURNAL

COMMENT

REFERENCE AUTHORS ٥,

source

FEATURES

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/dev stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="AtJMT-overexpressing transgenic rice lambda
phage cDNA library (JMT1)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Anoi; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site. mRNA was
prepared from Arabidopsis Jasmoinate Carboxyl
methyltransferase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CF921234 10-bp mRNA linear BST 05-NOV-2003 gmrhRww3-07_B06_1_046 Soybean root hair subtracted cDNA library gmrhRww3 Glycine max cDNA, mRNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 10)
Scheffler,B.E., Huang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.
Expressed sequence tags from soybean root hair subtractive cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
|cultivar="Williams 82"
|db_xref="taxon:3847"
|tissue_type="root hairs"
|clone_lib="Soybean root hair subtracted cDNA library
                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-4752
Fax: 573-882-0588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .10
/organism="Glycine max"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: staceyg@missouri.edu
Single pass sequence
Seq primer: T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CF921234.1 GI:38192028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycine max (soybean)
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Unpublished (2003)
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                                                                                                                                                                                                                                                          Query Match
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E 1 (bases 1 to 9)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.1., Kim,J.K., Kim,Y.-K. and Nahn,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 331 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="JMT1--03-L16"
/tissue_type="leaf"
/tdov_tage="leaf"
/dov_tage="leaf"
/lab_host="B_COII SOLR"
/clone_lib="AtJMT-overexpressing transgenic rice lambda
phage_cDNA_library (JMT1) " SK(+); Site_1: BCORI; Site_2:
Xho!, CDNA_was inserted into lamda Uni-ZAP XR vector at S'
end with ECORI and 3' end with Xho! site. mRNA was
prepared from Arabidopsis Jasmoinate Carboxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CF325619
9 bp mRNA linear EST 18-AUG-2003 JMT1--03-L16.gl AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-L16, mRNA
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1 (bases 1 to 9)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongln, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Query Match

O.3%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    methyltransferase overexpression line.
                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
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/tissue_type="leaf"
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CF325619.1 GI:33799518
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ORGANISM
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                             AUTHORS
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ORGANISM

SOURCE

ACCESSION VERSION KEYWORDS TITLE JOURNAL COMMENT

FEATURES

REPERENCE AUTHORS

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/organism="Descurainia sophia"
/mol_type="mRNA"
/db_xref="teaxon:89411"
/clone="boot" ole11"
/tissue_type="l-month seedlings - 1 cm tall - 8 leaf"
/clone_lb="Ds01_AAFC_ECORC_cold_stressed_Flixweed_seedlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CF543031 11 bp mRNA linear EST 22-SEP-2003 S015532-024-030-P02-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone 024-030-P02 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: Bluescript SK+/Xhol-EcoRI, Site 1: Eco RI; Site 2: Xho I; Plants were grown for 1 month at 200C/16 Ns: Iight/day (average 8 leaves, 1 cm tall, weight 0.02g/plant). Then they were exposed to 20C, 12 hrs light/day, for 1 week. Library prepared by C. Piche using Stratagene kit."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophylalaes; Amaranthaceae; Beta.

[ (bases 1 to 11) Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Radelof, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide
Fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
            Bastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KlA
OC6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1601
Email: singhia@em.agr.ca.
Location/Qualifiers
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/cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 87.5%; Pred. No. 87; Conservative 0; Mismatches 1; Indels
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ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
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Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 11 Std Error: 0.00
Plate: 30 row: P column: 02
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/db_xref="taxon:161934"
/clone="024-030-p02"
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/ Organism="Nicotiana benthamiana"

/ mol_type="mRNa"

/ db_xref="taxon:4100"

/clone="NBMDJ48"

/tissue_type="abiotic and biotic stress-treated leaves,

/clone="NBMDJ48"

/tissue_type="abiotic and biotic stress-treated leaves,

/clone_lib="Nicotiana benthamiana mixed tissue cDNA

library, normalized, full-length"

/ clone_lib="Nicotiana benthamiana mixed tissue cDNA

library, normalized, full-length"

/ note="Vector: pCWNgort6.1" Site 1: Site 2: Not1;

supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture

grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),

cold-stressed leaves (5 C 3 hr, 6hr), and pathogen

challenged leaves (Pseudomonas syringae pv tomato 12 hr;

Xanthomonas campestris pv campestris 12 hr, labr;

Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas

campestris pv vesicatoria 18hr). RNA was isolated from

less tissues and pooled in approximately equal molar
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                                                                                                                                                               Sukaryotes, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanaceae; Nicotiana.

1 (bases 1 to 10)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B., Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana (Dupublished (2003)

Other_ESTS: EST761693

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr. Rockville, MD 20850, USA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Descurainia.
1 (bases 1 to 11)
Singh,J.A., Piche,C., Couroux,P., De Moors,A., Harris,L.J.,
Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker,N.A.
Expressed Sequence Tags from Cold-Stressed Descurainia sophia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: GTA ATA CGA CTC ACT ATA GGG C.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.3%; Score 6.4; DB 1; Length 10; 87.5%; Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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                                                       CK298980.1 GI:39886896
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                                                                                                                 Nicotiana benthamiana
Nicotiana benthamiana
mRNA sequence.
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Unpublished (2001)
Contact: Singh, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Descurainia sophia
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Best Local Similarity 87.5
Matches 7; Conservative
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RESULT 157 BU238234/c DEFINITION

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ORGANISM

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COMMENT

TITLE

ACCESSION VERSION KEYWORDS

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Gaps .,

Query Match

DEFINITION

ACCESSION VERSION KEYWORDS

RESULT 159

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CF338362

ORGANISM

SOURCE

REFERENCE AUTHORS

TITLE JOURNAL

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Usyas sativa

Ewkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Epkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Epkartophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartcideae; Oryzaa.

CE 1 (bases I to 8)

RS Kim, J.S., Jun, K.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTS

IML Umpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

Localon/Qualifiers
                                                                                          CF339016 8 bp mRNA linear EST 18-AUG-2003 RCL1--03-I11.91 Regenerated callus lambda phage cDNA library (RCL1) Oryza sativa cDNA clone RCL1--03-I11, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBluescript SK(+); Site_1: SstI; Site_2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on
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RCL1--05-K22.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa cDNA clone RCL1--05-K22, mRNA sequence.
CF339699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="callus"
/dev stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enrhartoideae; Oryzeae; Oryza. Liliopsida; Poales; Poaceae; Enrhartoideae; Oryzeae; Oryza. Liliopsida; Li Chases I to 8)
Kim,J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clome lib="Regenerated callus lambda phage cDNA library (RCL1)"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RCL1--03-I11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regenerated media"
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                                      RESULT 160
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                                                                                                            DEFINITION
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/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-leaf"
/note="Vector: PGWVSPORT6; Site_1: Sall; Site_2: NotI;
cDNA_library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                    0
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I (bases 1 to 8)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Contact: Nahm B.H.
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                                                                                                                                                                                     Note:
                                                                                                                                                                     SP6-SAII-CCACGCCTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yopidn, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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Location/Qualifiers
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100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                           Score 6.2; DB Pred. No. 90; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="RCL1--01-H06"
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Matches 6; Conserval
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Matches 8; Conserv
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source

FEATURES

Contact: Nahm B.H.

AAGCTG 7

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1. (Dases 1 to 8)
Alkharouf,N.W., Khan,R. and Matthews,B.F.
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode (2002)
induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"
                                                                                                                                                                                                                                                                                                                                CA850825

B bp mRNA linear EST 01-AUG-2003
D06H10 H10 16.abl cDNA Peking library 2, 4 day SCN3 Glycine max
CDNA clone D06H10 5', mRNA sequence.
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8 bp mRNA linear EST 01-AUG-2003
D06H10 H10_16.abl cDNA Peking library 2, 4 day SCN3 Glycine max
cDNA clone D06H10 5', mRNA sequence.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Glycine max
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contract: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/cullivar="Peking"
/db_rare="beking"
/db_rare="beking"
/clome="boking"
/tissue_type="Roots"
/dow_stage="Seedlings"
/dow_stage="Seedlings"
/clome_lb="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."
                                                                                                                          Gaps
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                                                                                                                     0; Indels
                                                                         DB 1; Length 8; 1.3e+02;
                                                                         0.3%; Score 6; DB 1
100.0%; Pred. No. 1.3
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: alkharon@ba.ars.usda.gov.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                CA850825.1 GI:33387618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:33387618
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                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
Tel: 301 504 5750
Fax: 301 504 5728
                                                                                                                                                                      2068 AAGCTG 2073
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                                                                                               Local Similarity
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Oryza sativa

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

E (bases 1 to 8)

S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBluescript SK(+); Site 1: S&LI; Site 2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with S&LI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CF340204 8 bp mRNA linear EST 18-AUG-2003 RCL1--07-E15.gl Regenerated callus lambda phage cDNA library (RCL1) Oryza sativa cDNA clone RCL1--07-E15, mRNA sequence.
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                                                                                                                                                                                                                                                                                                /tissue type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
(RCL)"
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/clone_lib="Regenerated callus lambda phage cDNA library
(RCL1)"
    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bloinformatics, MyongJi University
Yorgin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Location/Qualifiers
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ilarity 100.0%; Pred. No. 1.3e+02;
Conservative 0; Mismatches 0;
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/organism="Oryza sativa"

    .8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"

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                                                                                                                                                                                                                                                            db_xref="taxon:4530"
clone="RCL1--05-K22"
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Best Local Similarity
6, Conserva
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/.organisme=.Oryza sativa"
//wolltype=!mRNA"
/cultivar="mackand"
/db_xref="taxor:4530"
/db_xref="taxor:4530"
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/lab_host="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                            CF297970
8 bp mRNA linear EST 15-AUG-2003 7LEAF--01-C16.gl Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--01-C16, mRNA sequence.
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8 bp mRNA linear EST 15-AUG-2003
7LEAF--01-C16.gl Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--01-C16, mRNA sequence.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Burhartoideae; Oryzae, Oryza.
1 (bases 1 to 8)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Kim, J.S., Jun, K.M., K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (1203)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bloscience and Bloinformatics, MyongJi University
           /clone_lib="cDNA Peking library 2, 4 day SCN3" /note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhrahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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0.3%; Score 6; DB 1; Ler
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                               0.3%; Score 6; DB 1
llarity 100.0%; Pred. No. 1.3
Conservative 0; Mismatches
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Best Local Similarity
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CF297970/c
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ORGANISM
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JOURNAL
COMMENT
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                                       Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Goybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
BAGG.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAB51350

B bp mRNA linear RST 01-AUG-2003
D12G08 N20_14.abl cDNA Peking library 2, 4 day SCN3 Glycine max
CDNA clone D12G08 5', mRNA sequence.
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Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
Unpublished (2002)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicocyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Roots"
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/dev stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."
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Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
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100.0%; Pred. No. 1.3e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                  Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                 'organism="Glycine max"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .8
/organism="Glycine max"
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Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
Location/Qualifiers
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/db_xref="taxon:3847"
/clone="D12G08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="D06H10"
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Best Local Similarity
Matches 6; Conserv
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                                            REFERENCE
AUTHORS
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8 bp mRNA linear EST 18-AUG-2003
NACL--06-F04.gI Rice callus plasmid cDNA library (NACL) Oryza
Eativa cDNA clone NACL--06-F04, mRNA sequence.
CF330558
CF330558.1 GI:33809354
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NACL--06-F04.gl Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--06-F04, mRNA sequence.
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/db xref="texcators"/
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/clone="NACL--06-F04"
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/clone lib="Rice callus plasmid cDNA library (NACL)"
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with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Brhartoideae; Oryzeae; Enhartoideae; Oryzeae; Oryza.

1. (Dases 1 to 8)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
Umpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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    Location/Qualifiers
                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                      0.3%; Score 6; DB 1; Length 8; 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.3e+02;
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                                                                                                                                                                     Conservative
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E (Dases 1 to 8)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6155
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea.

Ehrhartoideae; Oryzeae; Oryzea.

Ehrhartoideae; Oryzeae; Oryzea.

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 230 6193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 bp mRNA linear EST 15-AUG-2003
HD--01-P12.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-P12, mRNA sequence.
CP313731.1 G1:33685492
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    Location/Qualifiers
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    Location/Qualifiers
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                                                                              AUTHORS
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/cultivar="mRNA"
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/clone lib="mice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoR1; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
KEYWORDS
SOURCE
ORGANISM
                                                                             REFERENCE
AUTHORS
                                                                                                                 TITLE
JOURNAL
COMMENT
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0; Gaps Query Match 0.3%; Score 6; DB 1; Length 8; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 6; Conservative 0; Mismatches 0; Indels

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246 GCTGTC 251

qq

Search completed: March 1, 2004, 15:41:46 Job time: 2 secs